

Table 42: Comparative Sequences relating to SAG 0764**SEQ ID NO. 4201: 2603 V/R STRAIN**

ATGGTAAAATTAGTATTTCGCACGCCACGGTGAATCTGAGTGGAATAAAGCTAACCTTTTC
 ACTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGG
 AAATTAATTCAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGT
 GCCATCAAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATAAAGCAGAA
 GCAGCTGAACAATTTGGTGTATGAGCAAGTTTCATATTTGGCGTCGTTTCATATGATGTATTG
 CCTCCAGATATGGCTAAAGATGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCA
 CTAGATGATTCTGTTATTCCAGATGCAGAAAAACCTAAAAGTTACTTTAGAGCGTGCTCTT
 CCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGGTGGT
 GCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAGATGATGAA
 ATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTCGAATTTGATGAAAAATTA
 AACCTTGTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4202: 090 STRAIN

GTAAAATTAGTATTTCGCACGCCACGGTGAATCTGAGTG
 GAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
 ATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAAC
 AACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 AATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAAT
 AAAGCAGAAGCAGCTGAACAATTTGGTGTATGAGCAAGTTTCATATTTGGCG
 TCGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATT
 CAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCA
 GATGCAGAAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA
 AGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGGTGGT
 CACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTC
 GATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 CGAATTTGATGAAAAATTAACCTTGTTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4203: A909 STRAIN

GTAAAATTAGTATTTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA
 AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 ATCATGGCGCTTAAACGAACGTCATTACGGTGGATTGACAGGAAAAATA
 AAGCAGAAGCAGCTGAACAATTTGGTGTATGAGCAAGTTTCATATTTGGCGT
 CGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATT
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
 ATGCAGAAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGGTGGT
 ACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 GAATTTGATGAAAAATTAACCTTGTTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4204: H36B STRAIN

GTAAAATTAGTATTTCGCACGCCACGGTGAATCTGAG
 TGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGA
 AAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAG
 GTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAA
 ACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGA
 AAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAA
 ATAAAGCAGAAGCAGCTGAACAATTTGGTGTATGAGCAAGTTTCATATTTGG
 CGTCGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACA
 TTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCC
 CAGATGCAGAAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGG
 GAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGGTGG
 TGCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGT
 CAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTT
 TTCGAATTTGATGAAAAATTAACCTTGTTTTCAGAAATATTACTTAGGTAA
 A

SEQ ID NO. 4205: 18RS21 STRAIN

GTAAAATTAGTATTTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA
 AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA
 AAGCAGAAGCAGCTGAACAATTTGGTGTATGAGCAAGTTTCATATTTGGCGT
 CGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATT
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
 ATGCAGAAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGGTGGT
 ACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 GAATTTGATGAAAAATTAACCTTGTTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4206: M732 STRAIN

GTAAAATTAGTATTTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA
 AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT

Table 42: Comparative Sequences relating to SAG 0764

TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA
 AAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGT
 CGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATTC
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
 ATGCAGAAAACTAAAAGTTACTTTAGAGCGTGCTCTTCCCTTCTGGGAA
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTGGTGC
 ACACGGTAACTCAATCCGTGCTCTTGTAAACATATCAAACAATTGTGAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCCTTGTTTTC
 GAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4207: COH1 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGG
 TGAATCTGAGTGGAAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
 CAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 ACAGGAAAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGT
 TCATATTTGGCGTCGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAG
 ATGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGAT
 TCTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCT
 TCCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
 TGTTTGTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAACATATC
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCC
 ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATT
 ACTTAGGTAAA

SEQ ID NO. 4208: CJB110 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGG
 TGAATCTGAGTGGAAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
 CAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 ACAGGAAAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGT
 TCATATTTGGCGTCGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAG
 ATGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGAT
 TCTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCT
 TCCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
 TGTTTGTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAACATATC
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCC
 ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATT
 ACTTAGGTAAA

SEQ ID NO. 4209: 1169NT STRAIN

AGTATTTCGCACGCCACGGTGAATCTGAGTGGAAATAAAGCTAACCTTTTCA
 CTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATT
 GATGCTGGGAAATTAATTCAAGCAGCAGGTATTGAGTTCGACCTTGCTTT
 TACATCAGTTCTTAAACGTGCCATCAAAACAATAACCTTGCCCTTGAAG
 CAGCTGATCAACTTTGGGTACCAGTTGAAAAATCATGGCGCTTGAACGAA
 CGTCATTACGGTGGATTGACAGGAAAAATAAAGCAGAAGCAGCTGAACA
 ATTTGGTGATGAGCAAGTTCATATTTGGCGTCGTTTCATATGATGTATTGC
 CTCCAGATATGGCTAAAGATGATGAACATTTCAGCACATACTGATCGTCGC
 TATGCTTCACTAGATGATTCTGTTATTCCAGATGCAGAAAACCTAAAAGT
 TACTTTAGAGCGTGCTCTTCCCTTTCTGGGAAGATAAAATTGCTCCTGCTC
 TTAAGATGGTAAAAATGTGTTTGTGGTGCACACGGTAACTCAATCCGT
 GCTCTTGTAAACATATCAAACAATTGTCAGATGATGAAATCATGGACGTT
 TGAAATTCCTAACTTCCCACCCTTGTTTTCGAATTTGATGAAAAATTAA
 ACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4210: M781 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGGT
 GAATCTGAGTGGAAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGA
 TCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
 AAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGT
 GCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGT
 ACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGA
 CAGGAAAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTT
 CATATTTGGCGTCGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAGA
 TGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATT
 CTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTT
 CCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGT
 GTTTGTTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAACATATCA
 AACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCA
 CCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATT
 CTTAGGTAAA

SEQ ID NO. 4211: JM930013 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGGTGAATCT
 GAGTGGAAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTC
 AGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAG

Table 42: Comparative Sequences relating to SAG 0764

CAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATC AAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGT TGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAA AAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATT TGGCGTTCGTTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGA ACATTTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTA TTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCCTTC TGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGT TGGTGACACCGGTAACCTCAATCCGTGCTCTTGTAAAACATATCAAACAAT TGTCAGATGATGAAATCATGACGTTGAAATTCCTAACTTCCCACCACTT GTTTTTCGAATTTGATGAAAAATTAAACCTTGTTCAGAATATTACTTAGG TAAA						
PRETTY of: /biotmp/msa63264.2{*} March 10, 2003 09:30 ..						
1 50						
msa63264.2{110_090}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_1169NT}	-----		-AGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_18RS21}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_2603}	atgg	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_CJB110}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_COH1}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_H36B}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_JM9130013}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_M732}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_M781}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
msa63264.2{110_A909}	---	gtaaaat	tAGTATTTCGC	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC
Consensus	***	-----	-*****	*****	*****	*****
51 100						
msa63264.2{110_090}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_1169NT}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_18RS21}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_2603}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_CJB110}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_COH1}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_H36B}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_JM9130013}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_M732}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_M781}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
msa63264.2{110_A909}	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCTTTCAGAA	AAAGGTACAC	
Consensus	*****	*****	*****	*****	*****	*****
101 150						
msa63264.2{110_090}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_1169NT}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_18RS21}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_2603}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_CJB110}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_COH1}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_H36B}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_JM9130013}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_M732}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_M781}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_A909}	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
Consensus	*****	*****	*****	*****	*****	*****
151 200						
msa63264.2{110_090}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_1169NT}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_18RS21}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_2603}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_CJB110}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_COH1}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_H36B}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_JM9130013}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_M732}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_M781}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_A909}	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
Consensus	*****	*****	*****	*****	*****	*****
201 250						
msa63264.2{110_090}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_1169NT}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_18RS21}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_2603}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_CJB110}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_COH1}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_H36B}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_JM9130013}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_M732}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_M781}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC	

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_A909}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	251				300
msa63264.2{110_1169NT}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_18RS21}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_2603}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_CJB110}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_COH1}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_H36B}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_JM9130013}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M732}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M781}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_A909}	GCTTaAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
Consensus	****_*****	*****	*****	*****	*****
msa63264.2{110_090}	301				350
msa63264.2{110_1169NT}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_18RS21}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_2603}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_CJB110}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_COH1}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_H36B}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_JM9130013}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M732}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M781}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_A909}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	351				400
msa63264.2{110_1169NT}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_18RS21}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_2603}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_CJB110}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_COH1}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_H36B}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_JM9130013}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M732}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M781}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_A909}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	401				450
msa63264.2{110_1169NT}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_18RS21}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_2603}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_CJB110}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_COH1}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_H36B}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_JM9130013}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M732}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M781}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_A909}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	451				500
msa63264.2{110_1169NT}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_18RS21}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_2603}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_CJB110}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_COH1}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_H36B}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_JM9130013}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M732}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M781}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_A909}	AACCTAAAAG	TTACTTTAGA	GCGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	501				550
msa63264.2{110_1169NT}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_18RS21}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_2603}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_CJB110}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_COH1}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_H36B}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_JM9130013}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA
msa63264.2{110_M732}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTTGGT	GCACACGGTA

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_M781}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_A909}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
Consensus	*****	*****	*****	*****	*****
551					
msa63264.2{110_090}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_1169NT}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_18RS21}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_2603}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_CJB110}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_COH1}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_H36B}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_JM9130013}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_M732}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_M781}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_A909}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
Consensus	*****	*****	*****	*****	*****
601					
msa63264.2{110_090}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_1169NT}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_18RS21}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_2603}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_CJB110}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_COH1}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_H36B}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_JM9130013}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_M732}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_M781}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
msa63264.2{110_A909}	ATCATGGACG	TTGAAATTCC	TAACCTCCCA	CCACTTGTTT	TCGAATTTGA
Consensus	*****	*****	*****	*****	*****
651					
msa63264.2{110_090}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_1169NT}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_18RS21}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_2603}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_CJB110}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_COH1}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_H36B}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_JM9130013}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_M732}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_M781}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
msa63264.2{110_A909}	TGAAAAATTA	AACCTTGTTT	CAGAAATATTA	CTTAGGTAAA	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 4212: 2603 V/R STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGKNVFGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4213: 090 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGKNVFGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4214: A909 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGKNVFGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4215: H36B STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGKNVFGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4216: 18RS21 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGKNVFGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4217: M732 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGKNVFGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4218: COH1 STRAIN

Table 42: Comparative Sequences relating to SAG 0764

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVL
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGNVFGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4219: CJB110 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVL
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGNVFGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4220: 1169NT STRAIN

VFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRAIKT
TNLALAEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
AKDDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGNVFGAHGN
SIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4221: M781 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVL
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGNVFGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4222: JM9130013 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVL
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLEALPFWEDKIAPALKDGNVFGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

PRETTY of: /biotmp/msa70722.2{*} March 10, 2003 09:33 ..

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1
msa70722.2{110_090} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD 50
msa70722.2{110_18RS21} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_2603} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_A909} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_CJB110} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_COH1} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_H36B} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_JM9130013} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M732} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M781} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_1169NT} ---VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
Consensus ---*****
51
msa70722.2{110_090} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA 100
msa70722.2{110_18RS21} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_2603} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_A909} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_CJB110} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_COH1} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_H36B} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_JM9130013} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_M732} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_M781} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
msa70722.2{110_1169NT} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
Consensus *****
101
msa70722.2{110_090} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN 150
msa70722.2{110_18RS21} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_2603} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_A909} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_CJB110} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_COH1} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_H36B} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_JM9130013} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_M732} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_M781} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_1169NT} AEQFGDEQVH IWRRSYDVL PDMADDEHS AHTDRRYASL DDSVIPDAEN
Consensus *****
151
msa70722.2{110_090} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI 200
msa70722.2{110_18RS21} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_2603} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_A909} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_CJB110} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_COH1} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_H36B} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_JM9130013} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_M732} LKVTLEALP FWEDKIAPAL KDGNVFGA HGNSIRALVK HIKQLSDDEI

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Table 42: Comparative Sequences relating to SAG 0764

msa70722.2{110_M781}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
msa70722.2{110_1169NT}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
Consensus	*****	*****	*****	*****	*****
	201		229		
msa70722.2{110_090}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_18RS21}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_2603}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_A909}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_CJB110}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_COH1}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_H36B}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_JM9130013}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M732}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M781}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_1169NT}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
Consensus	*****	*****	*****		

Table 43: Comparative Sequences relating to SAG0079**SEQ ID NO. 4301: 2603 V/R STRAIN**

ATGAATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTAAGCAAGCAGCTAAGATC
 GTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCT
 AATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCT
 GATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAA
 GGTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCCTTAGATGCTACG
 CTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGT
 CTTATAGAGCGTTTGAGTGKTCGTATTATCAATCGTAAAACTGGTGAACTTTCCACAAA
 GTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAG
 CCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCATTCTTGAA
 CACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTT
 TTTGCAGATGTTGAAAAAGCGTTGCTAGAACTCAA

SEQ ID NO. 4302: 090 STRAIN (reverse complement)

AATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTAAGCAAGCAGCTAAGATC
 AGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCG
 CGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGG
 TGAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGA
 TATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGC
 CTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGT
 GGATCCATCATGTCTTATAGAGCGTTTGAGTGGTTCGTATTATCAATCGTAAAACTGGTGA
 AACTTTCCACAAAAGTGTTCACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACG
 TGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGA
 ACCATTCTTGAACACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGA
 AATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4303: 1169NT STRAIN (REVERSE COMPLEMENT)

TGGTAAAGGGACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCGCACATCTCAAC
 AGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAG
 TTATATTGATAAAGGTGAATTGGTTCCTGATCAAGTAACAAACGGGATTGTAAAGAGCG
 CTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTGATGGGTATCCACGTACTAT
 TGAACAAGCACACGCCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGT
 TATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGGTTCGTATTATCAA
 TCGTAAAACTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTAGATTATAAAGAAGA
 AGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTCA
 TATTGCTCAAGGAGAACCATTCTTGAACACTATAGTAAGCTTGGCCTTGTTACAGATAT
 TGAAGGTAATCAAGAAATAA

SEQ ID NO. 4304: 18RS21 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACCACGGGTTTCGCTGGTGCTGGTAAAGGTAAGCAAGCAGCTAAGATCG
 TTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTA
 ATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTG
 ATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAG
 GTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCCTTAGATGCTACGC
 TTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTC
 TTATAGAGCGTTTGAGTGGTTCGTATTATCAATCGTAAAACTGGTGAACTTTCCACAAAG
 TGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGC
 CTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCATTCTTGAAC
 ACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTT
 TTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4305: A909 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTAAGCAAGCAGCTAAGATCG
 CTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCG
 CAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAAT
 TGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCG
 CAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCCTTAG
 ATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATC
 CATCATGTCTTATAGAGCGTTTGAGTGGTTCGTATTATCAATCGTAAAACTGGTGAACTT
 TCCACAAAGTGTTCACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAG
 ATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAATCTA
 TTCTTGAACACTATCGAAAGCTTGGTCTTGTTACAGATATTGAAGGTAA

SEQ ID NO. 4306: CJB110 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACCACGGGTTTGCCTGGTGCTGGTAAAGGTAAGCAAGCAGCTAAGATCG
 GATCGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAAT
 GGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGT
 TCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGA
 AAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCCTTAGATGC
 TACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATC
 ATGTCTTATAGAGCGTTTGAGTGGTTCGTATTATCAATCGTAAAACTGGTGAACTTTCCA
 CAAAGTGTTCACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGA
 TAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCATTCTT
 TGAACACTATAG

SEQ ID NO. 4307: COH1 STRAIN (REVERSE COMPLEMENT)

ATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTAAGCAAGCAGCTAAGATGTTG
 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATC
 AAACCAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATG
 AAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTT
 TTTTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCCCTTAGATGCTACGCTTG
 AAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCAACATGCCTTA
 TAGAGCGTTTGAGTGGCGTATTATCAATCGTAAAACTGGTGAACTTTCCACAAAGTGT

Table 43: Comparative Sequences relating to SAG0079

TCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTG
AAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCATTCTTGAACACT
ATCGTAAGCTTGGTCTTGGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTG
CAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4308: H36B STRAIN (REVERSE COMPLEMENT)

CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAA
GTTATATTGATAAAGGTGAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGC
GCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTA
TTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTG
TTATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGGTCTGATTATCA
ATCGTAAACTGGTGAAACTTTCCACAAAGTGTTCACCCACCAGTAGATTATAAAGAAG
AAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTA
ATATTGCTCAAGGAGAATCTATTCTTGAACACTATCGTAAGCTTGGTCTTGGTTACAGATA
TTGAAGGTAATCAAGAAATAACAGAAGTTTTTGAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4309: JM9130013 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCTGGTGTCTGGTAAAGGT
ACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTCTCACATCTCAACAGGGGATATG
TTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGAT
AAAGGTGAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAG
GATGATATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCA
CACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATTAATATT
AAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGGTCTGATTATCAATCGTAAACT
GGTGAAGCTTTCCACAAAGTGTTCACCCACCAGTAGATTATAAAGAAGAAGATTACTAT
CAACGTGAAGATGATAAGCCTGAAACTGTTAAACGTCGCTTGGACGTTAATATTGCTCAA
GGAGAACCCTATTCTTGAACACTATAAAAAGCTTGGTCTTGGTTACAGATATTGAAGGTAAT
CA

SEQ ID NO. 4310: M732 STRAIN (REVERSE COMPLEMENT)

CTTTAATTATGGGTTTGCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATTGTTGAA
GAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAA
ACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATGAA
GTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTT
TTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCCTTAGATGCTACGCTTGAA
GAAGTGGATGCTACGCTTAGATGGTGTATTATTAATATTAAAGTGGATCCAACATGCCTTATA
GAGCGTTTGAGTGGCCGTATTATCAATCGTAAACTGGTGAAGCTTTCCACAAAGTGTTC
AACCACCAAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAA
ACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCCTATTCTTGAACACTAT
CGTAAGCTTGGTCTTGGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCA
GATGTTGAAAAAGCGTTG

SEQ ID NO. 4311: M781 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTACGGGTTTGCTGGTGTCTGGTAAAGGTACTCAA
GCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCG
GCCGCAATGGCTAATCAAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGT
GAATTTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGAT
ATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCC
TTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATTAATATTAAAGTG
GATCCAACATGCCCTTATAGAGCGTTTGAGTGGCCGTATTATCAATCGTAAACTGGTGAA
ACTTTCCACAAAGTGTTCACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGT
GAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAA

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25038.2{*} April 17, 2002 08:53 ..
PRETTY of: /biotmp/msa252229.2{*} January 31, 2003 03:05 ..

	1		50
msa252229.2{114_COH1}	----atcttt	taattatggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_M732}	-----cttt	taattatggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_M781}	---Aatcttt	taattacggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_A909}	---Aatcttt	taattatggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_JM9130013}	---Aatcttt	taattatggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_CJB110}	---Aatcttt	taaccacggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_090}	---Aatcttt	taattatggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_2603}	atgAatcttt	taattatggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_H36B}	-----	-----	-----
msa252229.2{114_18RS21}	---Aatcttt	taaccacggg	tttgccctggg gctggtaaag gtactcaagc
msa252229.2{114_1169NT}	-----	-----	---tggtaaag ggactcaagc
Consensus	****	-----	-----
	51		100
msa252229.2{114_COH1}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_M732}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_M781}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_A909}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_JM9130013}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_CJB110}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_090}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_2603}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_H36B}	-----	-----	-----
msa252229.2{114_18RS21}	agctaagatt	gttgaagaat	ttgggtgttg tcacatctca aCAGGGGATA
msa252229.2{114_1169NT}	agctaagatt	gttgaagaat	ttgggtgttg gcacatctca aCAGGGGATA

Table 43: Comparative Sequences relating to SAG0079

Consensus	-----	-----	-----	-----	*****
	101				150
msa252229.2{114_COH1}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_M732}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_M781}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_A909}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_JM9130013}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_CJB110}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_090}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_2603}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_H36B}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_18RS21}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
msa252229.2{114_1169NT}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa252229.2{114_COH1}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_M732}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_M781}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_A909}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_JM9130013}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_CJB110}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_090}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_2603}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_H36B}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_18RS21}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT
msa252229.2{114_1169NT}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATcAAGTAA	CAAACGGGAT
Consensus	*****	*****	*****	***-*****	*****
	201				250
msa252229.2{114_COH1}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_M732}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_M781}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_A909}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_JM9130013}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_CJB110}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_090}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_2603}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_H36B}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_18RS21}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
msa252229.2{114_1169NT}	TGTAAGAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC
Consensus	*****	*****	*****	*****	*****
	251				300
msa252229.2{114_COH1}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_M732}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_M781}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_A909}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_JM9130013}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_CJB110}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_090}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_2603}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_H36B}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_18RS21}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
msa252229.2{114_1169NT}	TTGATGGgTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG
Consensus	*****-**	*****	*****-****	*****	*****
	301				350
msa252229.2{114_COH1}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_M732}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_M781}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_A909}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_JM9130013}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_CJB110}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_090}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_2603}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_H36B}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_18RS21}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
msa252229.2{114_1169NT}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa252229.2{114_COH1}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA
msa252229.2{114_M732}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA
msa252229.2{114_M781}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA
msa252229.2{114_A909}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
msa252229.2{114_JM9130013}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
msa252229.2{114_CJB110}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
msa252229.2{114_090}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
msa252229.2{114_2603}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGk	tCGTATTATC	AATCGTAAAA
msa252229.2{114_H36B}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
msa252229.2{114_18RS21}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA

Table 43: Comparative Sequences relating to SAG0079

msa252229.2{114_1169NT}	TCCATCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
Consensus	*****-*****	*****	*****-*****	*****	*****
401					
msa252229.2{114_COH1}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M732}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M781}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_A909}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_JM9130013}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_CJB110}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_090}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_2603}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_H36B}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_18RS21}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_1169NT}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa252229.2{114_COH1}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_M732}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_M781}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_A909}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_JM9130013}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_CJB110}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_090}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_2603}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_H36B}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_18RS21}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
msa252229.2{114_1169NT}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TCAAACGTCG
Consensus	*****	*****	*****	*****	*-*****
501					
msa252229.2{114_COH1}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M732}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M781}	CTTGGACGTT	aATATTGCTC	AA-----	-----	-----
msa252229.2{114_A909}	CTTGGACGTT	aATATTGCTC	Aaggagaatc	tattcttgaa	cactatcgaa
msa252229.2{114_JM9130013}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactataaaa
msa252229.2{114_CJB110}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatag--
msa252229.2{114_090}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_2603}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_H36B}	CTTGGACGTT	aATATTGCTC	Aaggagaatc	tattcttgaa	cactatcgta
msa252229.2{114_18RS21}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_1169NT}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatagta
Consensus	*****	*****	**-----	-----	-----
551					
msa252229.2{114_COH1}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M732}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	agcttggtct	tggtacagat	attgaaggta	a-----	-----
msa252229.2{114_JM9130013}	agcttggtct	tggtacagat	attgaaggta	atca-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_2603}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_H36B}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_18RS21}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_1169NT}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aa-----
Consensus	-----	-----	-----	-----	-----
601					
msa252229.2{114_COH1}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M732}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	-----	-----	-----	-----	-----
msa252229.2{114_JM9130013}	-----	-----	-----	-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_2603}	tttgcagatg	ttgaaaaagc	gttgctagaa	ctcaaa	-----
msa252229.2{114_H36B}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_18RS21}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_1169NT}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----*****	*****	-----
636					

SEQ ID NO. 4312: 2603 V/R STRAIN

MNLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP
DEVINGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCL
LIERLSXRIINRKTGETFHKVFNPVVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILE
HYRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4313: 090 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPVVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH

Table 43: Comparative Sequences relating to SAG0079

YRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4314: 1169NT STRAIN

GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPDQVTNGIVKER
 LAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRIIN
 RKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEHYSKLG LVTDI
 EGNQEI

SEQ ID NO. 4315: 18RS21 STRAIN

NLLTTGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPSCL
 IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
 YRKLGLVTDIEGNQEITEVFADVEKALLE

SEQ ID NO. 4316: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPSCL
 IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGESILEH
 YRKLGLVTDIEG

SEQ ID NO. 4317: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPSCL
 IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGESILEH
 YRKLGLVTDIEG

SEQ ID NO. 4318: CJB110 STRAIN

NLLTTGLLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPSCL
 IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
 Y

SEQ ID NO. 4319: COH1 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPDE
 VTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPTCLI
 ERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
 RKLGLVTDIEGNQEITEVFADVEKALL

SEQ ID NO. 4320: H36B STRAIN

GDMFRAAMANQTEMGR LAKSYIDKGELVPDEV TNGIVKERLAEDDIAEKGFLLDGYPR TIE
 QAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRIINRKTGETFHKVFNPPVDYKEE
 DYYQREDDKPETVKRRLDVNIAQGESILEHYRKLGLVTDIEGNQEITEVFADVEKAL

SEQ ID NO. 4321: JM9130013 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPSCL
 IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
 YKKG LVTDI EGN

SEQ ID NO. 4322: M732 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPDE
 VTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPTCLI
 ERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
 RKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4323: M781 STRAIN

NLLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPTCL
 IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQ

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa32357.2{*} April 17, 2002 09:17 ..

	1				50
msa252352.2{114_18RS21}	-nllttgspg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_M781}	-nllitglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGR LAK
msa252352.2{114_CJB110}	-nllttgllg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_090}	-nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_JM9130013}	-nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_A909}	-nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_1169NT}	-----	-gkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_2603}	mnllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGR LAK
msa252352.2{114_COH1}	--llimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGR LAK
msa252352.2{114_M732}	--llimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGR LAK
msa252352.2{114_H36B}	-----	-----	-----	~GDMFRAAMA	NQTeMGR LAK
Consensus	*-----	-----	-----	*****	*****
	51				100
msa252352.2{114_18RS21}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR T	IEQAHALDAT
msa252352.2{114_M781}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR T	IEQAHALDAT
msa252352.2{114_CJB110}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR T	IEQAHALDAT

Table 43: Comparative Sequences relating to SAG0079

msa252352.2{114_090}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_JM9130013}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_A909}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_1169NT}	SYIDKGELVP	DqVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_2603}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_COH1}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_M732}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_H36B}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
Consensus	*****	*-*****	*****	*****	*****
101					
msa252352.2{114_18RS21}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_M781}	LEELGLRLDG	VINIKVDPTC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_CJB110}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_090}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_JM9130013}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_A909}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_1169NT}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_2603}	LEELGLRLDG	VINIKVDPsC	LIERLSxRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_COH1}	LEELGLRLDG	VINIKVDPTC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_M732}	LEELGLRLDG	VINIKVDPTC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
msa252352.2{114_H36B}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPPVDYKE
Consensus	*****	*****-*	*****-***	*****	*****
151					
msa252352.2{114_18RS21}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M781}	EDYYQREDDK	PETVKRRLDV	nIAQ-----	-----	-----
msa252352.2{114_CJB110}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hy-----	-----
msa252352.2{114_090}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_JM9130013}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hykklglvtd	iegn-----
msa252352.2{114_A909}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	ieg-----
msa252352.2{114_1169NT}	EDYYQREDDK	PETVKRRLDV	hIAQgepile	hysklglvtd	iegnqei---
msa252352.2{114_2603}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_COH1}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M732}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_H36B}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	iegnqeitev
Consensus	*****	*****	***------	-----	-----
201					
msa252352.2{114_18RS21}	fadvekalle	--			
msa252352.2{114_M781}	-----	--			
msa252352.2{114_CJB110}	-----	--			
msa252352.2{114_090}	fadvekalle	LK			
msa252352.2{114_JM9130013}	-----	--			
msa252352.2{114_A909}	-----	--			
msa252352.2{114_1169NT}	-----	--			
msa252352.2{114_2603}	fadvekalle	LK			
msa252352.2{114_COH1}	fadvekal-	--			
msa252352.2{114_M732}	fadvekalle	LK			
msa252352.2{114_H36B}	fadvekal-	--			
Consensus	-----	**			
212					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SEQ ID NO. 4401

STRAIN 2603

GTGGATAAACATCACTCAAAAAAGGCTATTTTAAAGTTAAACA
 CTTATAACAACCTAGTATTTTATTAATGCATAGCAATCAAGTGAATGCAGAGGAGCAAGAA
 TTAAAAAACCAAGAGCAATCACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCG
 GTAACCTACTAATCTGTTGAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAAGATGAATTATTAGAAGAG
 TTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAGAATATCCCTCT
 AAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAAATGCTTCAACTGCAATA
 GCACAGAAAGTTCCCTCAGCATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCT
 GTTCTTGATACATCTAAAAATAACAAATTACAAGCCATAACCCAAAGAGGAAAGGGAAAT
 GTAGTAGCTATTATTGATCTGGCTTTGATATTAAACCATGATATTTTTCGTTTAGATAGC
 CCAAAAGATGATAAGCACAGCTTTAAACTAAGACAGAATTTGAGGAATTTAAAGCAAAA
 CATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTTTTTGCACATAACTACGCC
 AACATACAGAAACGGTGGCTGATATTGCAGCAGCTATGAAAGATGGTTATGGTTTCAGAA
 GCAAAGAATATTTTCGATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGT
 CCAGCAATCAATGGTCTTCTTTTGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATG
 CGTATTCAGATAAAAATTGATTCCGACAAATTTGGTGAAGCATATGCTAAAGCAATCACA
 GACGCTGTTAATCTAGGAGCAAAAACGATTAAATATGAGTATTGGAAAAACAGCTGATTCT
 TTAATTGCTCTCAATGATAAAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTT
 GCAGTTGTTGTTGGCTGCCGAAATGAAGGCGCATTTGGTATGGATTATAGCAAAACCATTA
 TCAACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGAGT
 GTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAACAACTATTGAAGGT
 AAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTTGACAAAGGTAAGGCCTACGAT
 GTGGTTTATGCCAATTATGGTGCAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAG
 ATTGCATTAAATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAACTACTCATGCTACA
 AATGCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTCTA
 ATTCTTACCCTGAATACCTGTGGGGATTATTAGTAAAGTAGATGGCGAGCGTATAAAA
 AATACTTCAAGTCAGTTAAACATTTAACCAGAGTTTGAAGTAGTTGATAGCCAAGGTGGT
 AATCGTATGCTGGAACAATCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGAT
 GTAACAGCTTCTGGCTTTGAAATTTATTTCTTCAACCTATAATAATCAATACCAACAATG
 TCTGGTACAAGTATGGCTTACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCAT
 TTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAATTGTCTAAA
 AACATCCTCATGAGCTCAGCAACAGCAATTATATAGTGAAGAGGATAAGGCGTTTATTCA
 CCACGTCAGCAAGGTGCAGGTGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTAT
 ATTACTGAAACGATGGCAAGCTAAAAATTAACTCTCAACGAATGGGAGATAAATTTGAT
 ATCAGAGTTACAATTATATAAATTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAAT
 GTAGCAACAGAAAGTAATTTCTCGTGAATAAGAAACACAAGTTGATTTACTATTGAT
 GCTAGTCAATTTAGTCAGAAATTAAAGAACAGATGGCAAATGGTTATTTCTAGAAGGT
 TTTGTACGTTTAAAGAAGCCAGGATAGTAAATCAGGAGTTAATGAGTATTCCTTTTGTA
 GGATTTAATGGTGAATTTTGCGAACTTACAAGCACTTGAACACCGATTATATAAGACGCTT
 TCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAAGACCAATTGGAGTAC
 AATGAATCAGCTCCTTTTGAAGCAACAACCTATACTGCCTTGTAAACACAATCAGCGTCT
 TGGGGCTATGTTGATTATGTCAAAAATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCA
 AAAAGAAATTATTTAGGAACTTTGAAGATAAGGTTGAGGATAAAACAATTCATCTTTTG
 GAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCAAATAAAGATGGAATAGG
 GACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTGCTCAAGTT
 CTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGTTTACCATCTTATCGTAAAAAT
 TTCCATAATAATCCAAAGCAAGTGATGGTCAATATCGTATGGATGCTCTTCAGTGGAGT
 GGTTTAGATAAGGATGGCAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTAC
 ACACCAGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTACT
 AAGTCACCAAATCTTCTTACAGAGCTCAGTTTGTATGAACTAATCGAACATTAAGCTTA
 GCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCGTTTACAATTAGTTTTATCTCAT
 GTTGTAAAAAGATGAAGAATATGGGGATGAGACTTCTTACCATTATTTCCATATAGATCAA
 GAAGGTAAAGTGACACTTCTTAAACCGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGAC
 CCTAAGGCCTTGACACTTGTGTGGGAAGATAAAGCTGGTAATTTTCGCAACGGTAAAAATTG
 TCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATAGTAATTTCTAAC
 AGTTTCAAATATTTTATAACTTGAAAAAAGAACCTATGTTTTATTTCTAAAAAAGAAAAA
 GTAGTAAACAAGAACTAGAAAGAAATAATATTAGTTAAGCCGCAAACTACAGTTACTACT
 CAATCATGTCTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC
 AATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAAC
 CATACCTTACCTAGTACATCAGATAGAGCAACGAATGGTCTATTTGTTGGTACTTTGGCA
 TTGTTATCTAGTTTACTTCTTTATTTGAAACCCAAAAAGACTAAAAATAATAGTAAA

SEQ ID NO. 4402

STRAIN 090

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAATTGCT
 AATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTGTTGAAAA
 AACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAAATGGGTG
 ATACATCTGTAAAAAATGACAAAACAGAAAGATGAATTATTAGAAGAGTTA
 TCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAGAATA
 TCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAA
 ATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAGAGGTG
 AAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTGATACATCTAAATAAC
 AAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAATGTAGTAGCTATTA
 TTGATACTGGCTTTGATATTAAACCATGATATTTTTCGTTTAGATAGCCCA
 AAAGATGATAAGCACAGCTTTAAACTAAAGCAGAATTCGAGGAATTTAAA
 AGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTTT
 TTGCACATAAATACTACGCCAACATAACAGAAACGGTGGCTGATATTGCAGCA
 GCTATGAAAGATGGTTATGGGTGAGAAAGCAAGAATATTTCGCATGGTAC
 ACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCAATCAATG
 GTCTTCTTTTGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATGCGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATTCCAGATAAAATTGATTCCGACAAATTTGGAGAAGCATATGCTAAAGC
 AATCACAGACGCTGtTAATCTAGGAGCAAAAaCGATTAAATATGAGCCTTG
 GAAAAACAGCAGATTCTTTAAttGCaCTCAATGATAAAAGTTAAATTAGCA
 CTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGAAA
 TGAAGGTGCATTTGGTATGGATTATAGCAAACATTATCAACTAATcCTG
 ACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTtTGAGTGTT
 GCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACAATAT
 TGaaGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTtGACA
 AAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAaAAAAAGAC
 TTTGAAGGTAAgGACtTTAAAGGTAAGATTGCATTAAAtGAGCGTGGtGG
 TGGACTTGATTTTATGACTAAaatCACTcATGCTACAAATGCAGGTGTTG
 tTGGTaTCGTTtATTtTtAACGAtCAAGAAaAACGtGGAAATTTTcTAATT
 CCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGATGGCGAGCG
 TATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTtgAAGTAG
 TTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGGGGCGTG
 ACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAAT
 TTATTCTTCAACCTATAATAATCAATACCAACAATGTCTGGTACAAGTA
 TGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCATTTG
 GCTGAGAAATATAAAGGGATGAATTTAgATTCTAAAAAATTGCTAGAATT
 GTCTAaAAACATCCTCATGAGCTCAGCaCAGCATTATATAGTgAAGAgG
 ATAAGGCGTtTtATTCaCCACGTCAGCAAGGtGCAGGtGTAGTTGATGCT
 GAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAGC
 TAAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGTTACAA
 TTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGTA
 GCAACAGAACaAGTAAATAAAGGTAAATTTGCCCTTAAACCACAAGCCTT
 GCTAGATACTAATTGGCAGaaAGTAATTCTTcGTGATAAAGAAACACAAG
 TTcGATTTTACTATTGATGCTAGTCAATTTAGTCAGAAATTTAAAGAACAG
 ATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTAAAGAAGCCAA
 GGATAGtAATCAGGAGTTAaTGAGTATTCTTtTGTTAGGATtAATGGTG
 ATTTTGCGAACCTTACAGCACCTTGAACACCGATTTATAAGACGCTTTCT
 AAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAAGACCAATT
 GGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACCTATACTGCCTTGT
 TAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAATGGTGGG
 GAGTTAGAATTAGCACCGGAgAGTcCAAAAAGAATTATTTTAgGAACTTT
 TGAGAATAAGGTTGAGGATAAAACAATTATCTTTTGGAAAGAGATGCAG
 CgAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGAAATAGGGAT
 GAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTGC
 TCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGTTTTAC
 CATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCAT
 TATCGTATGGATGCCCTTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAGT
 TGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGTAGCAG
 AAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAAG
 TCACCAATCTTCTTTACTAGCTCAGTTTGATGAACTAATCGAACATT
 AAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATATCGTTTAC
 AATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATGAGACT
 TCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCTTAA
 AACGGTTAAGATAGGAGAGAGTGAAGTTGCAGTAGACCTAAGGCCTTGA
 CACTTGTGTGGAAAGATAAAGCTGGTAATTTTGCAACGGTAAATTTGTCT
 GACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAAT
 TTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAGAACTATGTTTA
 TTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAATAACATTA
 GTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTAAAGAAATAAC
 TAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAGTAGCA
 GAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCAT
 ACC

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STRAIN A909

GAGGAGCAAGAATTAAAAAACCAAGAGCAAT
 CACCTGTAATTGCTAATGTGTCAACAGCCATCGCCATCGGTAACTACT
 AATACTGTTGAAAAACATCTGTAACATCTGCTTCTGCTAGTAATACAGC
 GAAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT
 TATTAGAAGAGTTATCTAAAAACCTTGATACGCTCTAATTTGGGGGCTGAT
 CTTGAAGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAG
 CAATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAG
 CATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGAT
 ACATCTAAAATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAA
 TGTAGTAGCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTTC
 GTTTAGATAGCCCAAAAGATgaTAAGCACAGCTTTTaaACTAAGGCAGAA
 TTTGAGGAATTAAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAA
 CGATAAGATTGtTTTGCACATAACTACGCCaCAATACAGAAACGGTGG
 CTGATATTGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAAGAAT
 ATTTTCGATGGTACACAGTGTGCTGGTATTTTGTAGGTAATAGTAAACG
 TCCAGCAATCAATGGTCTTCTTTTGAAGGTGCAGCGCCAAATGCTCAAG
 TCTTATTAAATGCGTATTCCAGATAAAATTGATTCCGACAAATTTGGTGAA
 GCATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAACGAT
 TAATATGAGCCTTGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATA
 AAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTT
 GTGGCTGCCGAAATGAAGGTGCATTGGTATGGATTATAGCAAACCAATT
 ATCAACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAG
 ATACTTTGAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTC
 GTTGAACAACCTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTC
 TAAACCTTtTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GTGCAAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATT
AATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTA
CAAATGCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGT
GGAAATTTTCTAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAA
AGTAGATGGCGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTAAACC
AGAGTTTGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAA
TCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGC
TTCTGGCTTTGAAATTTATTCTTCAACCTATAATAATCAATACCAACAA
TGTCTGGTACAAAGTATGGCTTCACCACATGtTGCAGGATTAAATGACAATG
CTTCAAAGTCATTGCGCTGAGaAATATAAAGGGATGAATTTAGATTCTAA
AAAATTGCTAGaATTGTCTAAAAACATcCTCATGAGCTCAGCAACAGCAT
TATATAGTGAAGAGGATAAGGCGTTTATTACCACGTCAGCAAGGTGCA
GGTGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGG
AAACGATGGCAAAGCTAAAAATTAATCTCAAACGAGTGGGAGATAAATTTG
ATATCACAGTTACAATTCAAACTTGTAGAAGGTGTCAAAGAATTGTAT
TATCAAGCTAATGTAGCAACAGAACAAAGTAAATAAAGGTAAATTTGCCCT
TaAAACCaCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTG
ATAAAGAAACACAAGTTCTGATTACTAeTGATTCTAGTCAATTTAGTCAG
AAATTAAAAGAACAGATGCGCAATGGTTATTTCTTAGAAGGTTTGTACG
TTTTAAAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTG
TAGGATTTAATGGTGATTTTGGCAACTTACAAGCACTTGAACACCGATT
TATAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAAC
TCATAAAGACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACA
ACTATACTGCCTTGTAAACACAATCAGCGTCTTGGGGCTATGTTGATTAT
GTCAAAAATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAT
TATTTTAGGAACTTTGTAGAAATAAGGTTGAGGATAAAACAATTCATCTTT
TGGAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAA
GATGGAAATAGGGATGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGT
TAAGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGC
AAAGTAAGGTTTTTACCATCTTATCGTAAAAAATTTCCATAATAATCCAAAG
CAAAGTGATGGTCATTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGA
TAAGGATGGCAAAGTTGTAGCAGATGGTTTATATACTTATCGTTTACGTT
ACACACCAGTAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTT
CAAGTAAGTACTAAGTCACCAATCTTCTTCACGAGCTCAGTTTGATGA
AACTAATCGAACATTAAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTT
CTACATATCGTCTACAATTAGTTTTATCTCATGTTGTAAGAGATGAAGAA
TATGGAGATGAGACTTCTTACCATTATTTCCATATAGATCGAGAAGGTAA
AGTGACACTTCTTAAACAGTTAAGATAGGAGAGAGTGAAGTTGCAGTAG
ACCCTAAGACCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTCCGA
ACGGTAAAAATGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGA
AAACGCTATAGTAATTTCTAACAATTTCAAATATTTTGATAACTTGAAAA
AAGAACCTATGTTTATTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTA
GAAGAAATAGCATTAGTTAAGCCGCAACTACAGTTACTACTCAATCATT
GTCTAAAGAAATAACTCAATCAGGAAATGAGAAAGTCTCACTTCTACAA
ACAATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGG
GATTCTGTTAACCATAACC

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STRAIN H36B

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAATTGC
TAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATACTGTTGAAA
AAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGCGAAAGAAATGGGT
GATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAGAGTT
ATCTAAAAACCTTGATACGCTAATTTGGGGGCTGATCTTGAAGAAGAAT
ATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACA
AATGCTTCAACTGCAATAGCACAGAAaGTTCCCTCAGCATATGAAGAGGT
GAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGATACATCTAAATAA
CAAAATTGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGCTATT
ATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGCCC
AAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAAATTTGAGGAATTAA
AAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTT
TTTGACATAACTACGCCaCAATACAGAAACGGTGGCTGATATTGCAGC
AGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAATATTTCGCATGGTA
CACAGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAATCAAT
GGTCTTCTTTTAGAAGGTGCAGCGCAAAATGCTCAAGTCTTATTAATGCG
TATTCAGATAAAATTGATTTCGGACAAATTTGGTGAAGCATATGCTAAAG
CAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAGCCTT
GGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATAAAGTTAAATTAGC
ACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGGA
ATGAAGGTGCATTTGGTATGGATTATAGCAAACATTATCAACTAATCCT
GACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGAGTGT
TGCTAGCTATGAATCACTTAAACTATCAGTGAGGTCGTTGAAACAATA
TTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTtTGAC
AAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAAAGA
CTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTGAGCGTGGTG
GTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAGGTGTT
GTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAATTTTCTAAT
TCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGCGAGC
GTATAAAAAATACTTCAAGTCAGTTAACATTTAAACAGAGTTTGAAGTA
GTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGGGGCGT
GACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAA
TTTATTCTTCAACCTATAATAATCAATACCAACAATGTCTGGTACAAGT
ATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCATTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAT
 TGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAG
 GATAAGGCGTTTTATTCCACCAGTCAGCAAGGTGCAGGTGTAGTTGATGC
 TGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAAG
 CTAAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGTTACA
 ATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGT
 AGCAACAGAACAAAGTAAATAAAGGTAAATTTGCCCTTAAACCaaAGCCT
 TGCTAGATACTAATTGGCAGAAAGTAAATTTCTCGTGATAAAGAAACACAA
 GTTCGATTIACCTATTGATTCTAGTCAATTTAGTCAGAAATTAAGAACA
 GATGGCAAATGGTTATTTCTTAGAAGGTTTGTACGTTTTAAAGAAGCCA
 AGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTAATGGT
 GATTTTGGCAACTtACAAGCACTTGAAACACCGATTTATAAGACGCTTTC
 TAAAGGTAGTTTCTACTATAAAACCAATGATACAACTCATAAAGACCAAT
 TGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATACTACTGCCCTG
 TTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAATGGTGG
 GGAGTTAgAATTAgCACCGGAGAGTCCAAAAAGAAATATTTTAGGAACCT
 TTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAGATGCA
 GCGAATAATCCATATTTTGGCATTCTCCAAATAAAGATGGAAATAGGGA
 TGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTG
 CTCAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGTTTTA
 CCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCA
 TTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAG
 TTGTAGCAGATGGTTTTTATACTTATCGTTTACGTTACACACCAGTAGCA
 GAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAA
 GTCACCAAATCTTCCTTCACGAGCTCAGTTTGTAGAACTAATCGAACAT
 TAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCGTCTA
 CAATTAGTTTTTATCTCATGTTGTAAAGATGAAGAATATGGAGATGAGAC
 TTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCCTA
 AAACAGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGACCTTAAGACCTTG
 ACACCTGTTGTGGAAGATAAAGCTGGTAATTTGCGCAACGGTAAATTTGTC
 TGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAA
 TTTCTAACAAATTTCAAATATTTTGATAACTTGAAAAAAGAACCTATGTTT
 ATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATAGCATT
 AGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAAATAA
 CTCAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATAGTAGC
 AGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCA
 TACC

SEQ ID NO. 4405

STRAIN 18RS21

GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACC

TGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATA
 CTGTTGAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCGAAA
 GAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATT
 AGAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTG
 AAGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAAT
 GTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATA
 TGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACAT
 CTAAAATAACAAAATTACAAAGCCATAACCCAAAGAGGAAAGGGAAATGTA
 GTAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTCTGTTT
 AGATAGCCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAATTTG
 AGGAATTAAAGCAAAACATAATATCACTTATGGGAAATGGGTAAACGAT
 AAGATTGTTTTTGCACATAACTACGCCAACAAACAGAAACGGTGGCTGA
 TATTGCAGCAGCTATGAAAGATGGTTATGGTTCAGAAGCAAAGAATATTT
 CGCATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTTCCA
 GCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTT
 ATTAATGCGTATTCCAGATAAAATGATTCCGACAAATTTGGTGAAGCAT
 ATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAAT
 ATGAGTATTGGAAAAACAGCTGATTCTTTAATTGCTCTCAATGATAAAGT
 TAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGG
 CTGCCGGAATGAAGGCGCAATTTGGTATGGATTATAGCAAACCATTTATCA
 ACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATAC
 TTTGAGTGTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTGCTTG
 AAACAATATTGAAGGTAAGGTTAGTTAAGTTGCCGATTGTGACTTCTAAA
 CCTTTTGACAAAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGC
 AAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTG
 AGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGTACAAAT
 GCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAA
 TTTTCTAATTCCTTACCGTGAATTACCTGTGGGGATTATTAgTAAAGTAG
 ATGGCGAGCGTATAAAAAATACCTTCAAGTCAGTTAACATTtAACCAgAGT
 TTTGAAGtAGTTGATAGCCAAGGTGGtAATCGTaTGCTGGAACAATCAAG
 TTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTG
 GCTTTGAAATTTATTTCTTCAACCTATAATAATCAATACCAaCAATGTCT
 GGTACAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCA
 AAGTCATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAAT
 TGCTAGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATAT
 AGTGAAGAGGATAAGGCGTTTTATTCCACCAGTCAGCAAGGTGCAGGTGT
 AGTTGATGCTGAAAAAGCTATCCAAGCTCaATATTATATTACTGGAAACG
 ATGGCaagCTAAATTAATCTCAAACGAATGGGAGATAAATTTGATATC
 ACAGTTACAATTCATaAACTTGTAAGAAGGTGTCAAAGAATTGTATTATCA
 AGCTAATGTAGCAACAGAACAAAGTAAATAAAGGTAAATTTGCCCTTaAAC
 CACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAAATCTTcGTGATAAA
 GAAACACAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTA
 AAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGA
 TTTAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACACCGATTTATAA
 GACGATTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATA
 AAGACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACATAT
 ACTGCCCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAA
 AAATGGTGGGGAGTTAGAATTAGCaCCGGAGAGTCCAAAAAGAATTATTT
 TAGGAACCTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGAA
 AGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGG
 AAATAGGGACGAAATCACTCCCCAGGCAACCTTCTTAAGAAATGTTAAGG
 ATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGT
 AAGGTTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAG
 TGATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGG
 ATGGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACA
 CCAGTAGCAGAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTACAAGT
 AAGTACTAAGTCACCAATCTTCTTCCAGAGCTCAGTTTGATGAAACTA
 ATCGAACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACA
 TATCGTTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGG
 GGATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGA
 CACTTCTTAAACCGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCT
 AAGGCCCTTGACACTTGTGTGGAAAGATAAAGCTGGTAATTTCCGCAACGGT
 AAAATTGTCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACG
 CTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAGAA
 CCTATGTTTTATTCTAAAAAAGAAAAAGTAGTAAACAAGAACTAGAGA
 AATAATATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTA
 AAGAAATAACTAAATCAGGAAATGAGAAAGTCTCCTCCTTCTACAAACAAT
 AATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCT
 TGTTAACCATACC

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STRAIN M732

GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCT
 GTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATAT
 TGTTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAAG
 AAATGGGTGATACATCTGTAAAAAATGACAAAAAGAGATGAATTATTA
 GAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGA
 AGAAGAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATG
 TAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATAT
 GAAGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATC
 TAAATAACAAAATTACAAGCCACAACCCAAAGAGGAAAGGGAATGTAG
 TAGCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTTCGTTTA
 GATAGCCCAAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAAATTGA
 GGAATTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTAAACGATA
 AGATTGTTTTTGCACATAACTACGCCAACAAATACAGAAACGGTGGCTGAT
 ATTCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAAGAAATATTT
 GCATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAG
 CAATCAATAGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTA
 TTAATGCGTATTCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATA
 TGCTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATA
 TGAGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTT
 AAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGC
 TGCCGGAAATGAAGGTGCATTTGGTATGGATTATAGCAAACCATATCAA
 CTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACT
 TTGAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGA
 AACCACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAAC
 CTTTGAACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCA
 AAAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTGAG
 CGTGGTGGTGGACTTGATTTTATGACTAAAAATCACTCATGCTACAAATGC
 AGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAAT
 TTCTAATTCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGAT
 GGCGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTT
 TGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTT
 GGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTTCTGGC
 TTTGAAATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGG
 TACAAGTATGGCTTCAACCATGTTGCAGGATTAATGACAATGCTTCAAA
 GTCATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTG
 CTAGAAATGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAG
 TGAAGAGGATAAGGCGTTTTATTCAACCGTCAGCAAGGTGCAGGTGTAG
 TTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACGAT
 GGCAAAGTTAAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCAC
 AGTTACAATTCACTAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAG
 CTAATGTAGCAACAGAAaCAAGTAAATAAAGGTAAATTTGCCCTTaACCA
 CAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATCTTCGTGATAAAGA
 AACACAAGTTGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAA
 AAGAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTGTACGTTTTAAA
 GAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATT
 TAATGGTGATTTTGCGAACCTACAAGCACTTGAAACaCCGATTTATAAGA
 CGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATAAA
 GACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACATAC
 TGCCTTGTAAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAA
 ATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTA
 GGAACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAG
 AGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATAGGGACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGAT
 ATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAA
 GGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTG
 ATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGAT
 GGCAAAGTTGTAGCAGATGGTTTATACTTATCGCTTACGTTACACACC
 AGTAGCAGAAGGAGCaAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAA
 GTACTAAGTCACCAATCTTCCTTCACGAGCTCAGTTTGTAGAACTAAT
 CGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATA
 TCGTTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGG
 ATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACA
 CTTCCCTAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCTAA
 GGCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAA
 AATTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGaAAACGCT
 ATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACC
 TATGTTTATTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAA
 TAACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAA
 GAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAA
 TAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTG
 TTAACCATAACC

SEQ ID NO. 4407

STRAIN COH1

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTaACTACTAATATTG
 TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
 ATGGGtgATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGA
 AGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAG
 AAGAATATCCCTCTAAACCAGAGaCAACCAACAATAAGAAAGCAATGTA
 GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTA
 AAATAACAAAATTACAAGCCACAACCCAAAGAGGAAAGGGAAATGTAGTA
 GCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCGTTTAGA
 TAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAATTGAGG
 AAtTAAAGCAAAACATAATATCACTTATGGGAAATGGGTAAACGATAAG
 ATTGTTTTTTGCACTAACTACGCCaCAATACAGAAACGGTGGCTGATAT
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAAGAATATTTTGC
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCCAGCA
 ATCAATAGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATT
 AATGCGTATTTCCAGATAAAATTTGATTCCGACAAATTTGGAGAAGCATATG
 CTAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAATATG
 AGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA
 ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTG
 CCGGAAATGAAGGTGCATTGTTGATGGATTATAGCAAACCATTATCAACT
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT
 GAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAAA
 CAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCT
 TtTGACAAAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAAA
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCG
 TGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAG
 GTGTTGTTGGTATCGTTATTTTAAAGATCAAGAAAAACGTGGAAATTTT
 CTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGATGG
 CGAGCGTATAAAAAATCTTCAAGTCAGTTAACATTAAACAGAGTTTTG
 AAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG
 GGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTTCTGGCTT
 TGAaATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA
 CAAGTATGGCTTACCACATGTTGCAGGATTAATGACAATGCTTCAAAGT
 CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAaAAAAATTGCT
 AGaATTGTCTAaAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG
 AAGAGGATAAGGCGTTTATTACACAGTCAGCAAGGTGCAGGTGTAGTT
 GATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGG
 CAAAGTTAAATTAATCTCAACGAGAGGGAGATAAATTTGATATCACAG
 TTACAATTCATaAATTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCT
 AATGTAGCAaCAGAACAGTAAATAAAGGTAATTTGCCCTTAAACCA
 AGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAAGAAA
 CACAAGTTGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAAA
 GAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTTAAAGA
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
 ATGGTGATTTTGGCACTTACAAGCACTTGAAACACCGATTATAAGACG
 CTTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACCTATAAAGA
 CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAATACTACTG
 CCTTGTAAACACAATCAGCGCTTTGGGGCTATGTTGATTATGTCAAAAAT
 GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGG
 aACTTTTGAGAAATAAGGTTGAGGATAAAACAATTCACTTTTGGAAAGAG
 ATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAAT
 AGGGACGAAATCACTCCCCAGGCaACTTTCTTAAGAAATGTTAAGGATAT
 TTCTGCTCAAGtCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGG
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAAGTGAT
 GGTCAATATCGTATGATGCTCTTCAGTGGAGTGGTTTAgATAAGGATGG
 CAAAGTTGTAgCAGATGGtTTTTATACTTATCGCTTACGTTACACACCAG
 TAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTaAAGTTCAAGTAAGT
 AcTAAGTCACCAATCTTCCTTCACGAGCTCAGTTTGTAGGaAACTAATCG
 AACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACATATC
 GTTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT
 TCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGG
 CCTTGACACTTGTGTGGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA
 TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
 AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCTA
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATA
 ACATTAGTTAAGCCTCAAACCTACAGTTACTACTCAATCATTTGTCTAAAGA
 AATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATA
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT
 AACCATACC

SEQ ID NO. 4408

STRAIN M781

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTG
 TTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
 ATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGA
 AGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAG
 AAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTA
 GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTA
 AAATAACAAAATTACAGCCACAACCCAAAGAGGAAAGGAAATGTAGTA
 GCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGA
 TAGCCCAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAATTTGAGG
 AATTAAAAGCAAACATAATATCACTTATGGGAAATGGGTAAACGATAAG
 ATTGTTTTTGCACATAACTACGCCAaCAATACAGAAACGGTGGCTGATAT
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAAGCAAGAATATTTTGC
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCCAGCA
 ATCAATAGTCTTCTTTAGAAGGTGAGCGCCAAATGCTCAAGTCTTATT
 AATGCGTATTCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATATG
 CTAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAAATATG
 AGCCTGGGAAAAACGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA
 ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTG
 CCGGAAATGAAGGTGCATTTGGTATGGATTATAGCAAaCCATTATCAaCT
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT
 GAGTGTGCTAGCTATGAATCACTtAAAACCTATCAGTGAGGTGTTGAAA
 CAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACtTCTAaACCT
 TTTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAA
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCG
 TGGTGGTGGACTTGATTTTATGACTAAATCACTCATGCTACAAATGCAG
 GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAATTTT
 cTAATTCCTTACCGTGAATTACCTGTGgGGGTTATTAGTAAAGTAGATGG
 CGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACAGAGTTTTg
 AAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG
 GCGGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
 TGAATTTTATTTCTCAACCTATAATAATCAATACTAAACAATGTCTGGTA
 CAAGTATGGCTTCAACCATGTTGCAGGATTAATGACAATGCTTCAAAGT
 CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCT
 AGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG
 AAGAGGATAAGGCGTTTTATTACCACGTCAGCAAGGTGCAGGTGTAGTT
 GATGCTGAAAAAGCTATCCAAGCTCAATATTTATGTTACTGGAACGATGG
 CAAAGTTAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCACAG
 TTACAAATCTAaaACTTGTAgAAGGTGTCAAAGAATTGTATTATCAAGCT
 AATGTAGCAaCAGAAACAAGTAAATAaAGGTAAATTTGCCCTTaAaCCaCA
 AGCCTTGCTAGATACTAATTGGCAGAAAGTaATTCTTcGTGATAAAGAAA
 CACAAGTTcGATTTACTAtTGATGCTAGTCAATTTAGTCAGAAATTAAAA
 GAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTAAAGA
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
 ATGGTGATTTTGCGAACtTACAAGCACTTGAAACACCGATTTATAAGACG
 CTTTCTAAAGGTAGTTTCTACTATAAaCCAAATGATACAACCTCATAAAGA
 CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTG
 CCTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAT
 GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGG
 AACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAG
 ATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAAT
 AGGGACGaaATCACTCCCCAGGCaActTTCTTAAGAAATGTTAAGGATAT
 TTCTGCTCAAGtTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGG
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAAGTGAT
 GGTCAATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGATGG
 CAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACCAG
 TAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGT
 ACTAAGTCACCAAATCTTCTTACGAGCTCAGTTTGATGAACTAATCG
 AACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACAtATC
 GTTTACAATTAGTTTTATCTCATGTTGTAAGAGATGAAGAATATGGGGAT
 GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT
 TCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGG
 CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA
 TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
 AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCTA
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATA
 ACATTAGTTAAGCCTCAAACCTACAGTTACTACTCAATCATTTGTCTAAAGA
 AATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATA
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AACCATACC

SEQ ID NO. 4409

STRAIN CJB110

GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGTAA
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATATTGTT
 GAAAAACATCTGTAnCAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT
 GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAG
 AGTTATCTAAAAACCTTGATACGTCTAATWTGGGGGCTGATCTTGAAGAA
 GAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGT
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAG
 AGGTGaAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAA
 ATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAATGTAGTAGC
 TATTATTGATACTGGCTTTGATATTAAACCATGATATTTTTCGTTTAGATA
 GCCCAAAGATGATAAGCACAGCTTTAAACTAAAGCAGAATTCGAGGAA
 tTAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGAT
 TGTTTTTGCACATAACTACGCCAACATAACAGAAACGGTGGCTGATATTG
 CAGCAGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTTCGCAT
 GGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCAAT
 CAATGGTCTTCTTTTGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAA
 TGCGTATTCCAGATAAAAATTGATTTCGGACAAATTTGGAGAAGCATATGCT
 AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAACGATTAATATGAG
 CCTTGGAACAGCAGATTCTTTAATTGCACTCAATGATAAAGTTAAAT
 TAGCACTTAAATTAGCTTcTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCC
 GGAAATGAAGGTGCATTTGGTATGGATTATAgCAAACCATTATCAACTAA
 TcCTGACTACGgtACGGTTAATAGTCCAGCTATTTcTGAAGATACTTTGA
 GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAACA
 ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTcTAAACCTTT
 TGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA
 AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTGAGCGT
 GGTGGTGGACTTGATTTTATGACTAAATCACTCATGCTACAAATGCAGG
 TGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTTc
 TAATTCCCTTACCGTGAATTACCTGTGgGGGTATTAGTAAAGTAGATGGC
 GAGCGTATAAAAAATACCTCAAGTCAGTTAACATTTAACCAGAGTTTGA
 AGTAgTTGATAGCCAAgGTGGCAATCGTATGCTGGAACAATCAAGTtGGG
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT
 GAAATTTATCTTCAACCTATAATAATCAATACCAACAATGTCTGGTAC
 AAGTATGGCTTCACCACATGtTGCAGGATTAATGACAATGCTTCAAAATC
 ATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTA
 GAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
 AGAGGATAAGGCGTTTTATTCCACCGTCAGCAAGGtGCAGGTGTAGTTG
 ATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGC
 AAAGCTAAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGT
 TACAATTCAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTA
 ATGTAGCAACAGAAACAAGTAAATAAAGGTAAATTTGCCCTTaAACACAA
 GCCTTGCTAGATACTAATTGGCAGAAAGTAATTCCTcGTGATAAAGAAAC
 ACAAGTTCGATTACTAtTGATGCTAGTCAATTTAgTCAGAAATTAAAG
 AACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTAAAGAA
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCTTTTGTAGGATTAA
 TGGTGATTTTGGCAACTtACAAGCACTTGAAACACCGATTATATAAGACGC
 TTTCTAAAGGTAGTtTCTACTATAAACCAATGATACAACCTCATAAAGAC
 CAATTGGAGTACAATGAATCAGCTCctTTTGAAAGCAACAACCTATACTGC
 CTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATG
 GTGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGGA
 ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCACTCTTTTGGAAGAGA
 TGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGAAATA
 GGGATGaaATCACTCCCCAGGCAACTTCTTAAGAAATGTTAAGGATATT
 TCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGT
 TTACCATCTTATCGTAAAAATTTCCATAATAATCCAAGCAAAAGTGATG
 GTCATTATCGTATGGATGCCTTTCAGTGGAGTGGTTTTAgATAAgGATGGC
 AAAGTTGTAGCAGATGGTTTTTACTTATCGCCTACGTTACACACCAGT
 AGCAGAAgGAGCAAAATAGTCAGGAGTCagACTTTAAAGTTCAAGTAAGTA
 CTAAGTCACCAAATCTTCTTTACTAGCTCAGTTTGATGAACTAATCGA
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCG
 TTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATG
 AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTT
 CCTAAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGACCCTAAGGC
 CTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTaAAAT
 TGCTGACCTCTTGAAaTAAGGCAGTAGTATCAGAGAAAGAAAACGCTATA
 GTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAAGAATCTAT
 GTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATAA
 CATTAGTTAAGCCGCAaACTACAGTTACTACTCAATCATTTGTCTAAAGAA
 ATAATAAATCAGGAAATGAGAAAGTCCCTCACTTCTACAAACAATAATAG
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
 ACCATACC

SEQ ID NO. 4410

STRAIN 1169NT

GAGGAGCAAGAATTAAAAAACCAAGAGCAATC
 ACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTA
 ATATGTTGAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATT
 ATTAGAAGAGTTATCTAAAAACCTTGATACGTCTAATATGGGGGCTGATC

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

TTGAAGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAGGAAAGC
 AATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGC
 ATATGAAGAGGTGAAGCCAAAAAGCAAGTCATCGCTTGCTGTTCTTGATA
 CATCTAAAATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAAT
 GTAGTAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTCG
 TTTAGATAGCCCAAAAGATGATAAGCACAGCTTTAAAAATAAGGCAGAAT
 TCGAGGAATTAAAAAGCAAAACATAATATCACTTATGGGAAATGGGTAAAC
 GATAAGATTGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGC
 TGATATTGCAGCAGCTATGAAAGATGGTTATGGTTTCAGAAGCAAAGAATA
 TTTTCGCATGGTACACACGTTGCTGGTATTtTTGTAGGTAATAGTAAACGT
 CCAGCAATCAATGGTCTTCTTTTAgAAGGTGCAGCGCCAAATGCTCAAGT
 CTTATTAATGCGTATTCCAGATAAAATtGATTTCGGACAAATTtGGAGAAG
 CATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCTaAAACGATT
 AATATGAGTATTGGAAAAACAGCTGATTCTTTAATTGCTCTCAATGATAA
 AGTTAAATTAgCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTG
 TGGCTGcCGGAAATGAAGGCGCATtGGTATGGATTATAGCAAACCGTTA
 TCAACTAATcCTGACTACGGtACGGtTAATAGTCCAGCTATTTCTGAAGA
 TACTTTGAGTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGG
 TTGAAACAACATTGAAGGTAAGTTAGTTAAGTtGCCGATTGtGACTTCT
 AAACCTTtGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATTATGG
 TGCAAAAAAGAGCTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAA
 TTGAGCGTGGTGGTGGACTTGATTtTATGACTAAAATCACTCATGCTACA
 AATGCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGG
 AAATTTTCTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAG
 TAGATGGCGAGCGTATAAAAaATACTTCAAGTCAGTTAACATTAAACAg
 AGATTtGAAGTAGTTGATAGCCAAgGTGGCAATCGTATGCTGGAACAATC
 aAGTtGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTT
 CTGGCTTCGaaATTTATTCTTCaaCCTATAATAATCAATACCAACAATG
 TCTGGTACAAGTATGGCTTCACCACATGTTGCAGGATTAAAGACAATGCT
 TCAAAGTCATTTGGCTGAGaAATATAAAGGGATGAATTTAgATTCTAaAA
 AATTGCTAGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATT
 TATAGTGAAGAGGATAAGGCGTTTATTTCACCACGTCAGCAAGGtGCAGG
 TGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAA
 ACGATGGCAAAGCTAAATTAATCTCAAACGAGTGGGAGATAAATTTGAT
 ATCACAGTTACAATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATT
 TCAAGCTAATGTAGCAACAGAACAGTAAATAAAGGTAATTTGCCCTTA
 AACCACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTCTGAT
 AAAGAAACACAAGTTCGATTACTATTGATGCTAGTCAATTTAgTCAGAA
 ATTAAAGAACAGATGGCAAAATGGTTATTTCTTAgAAGGTTTGTACGTT
 TTAAAGAAGCTAAGGATAGTAATCAGGAGTTAATGAGTATTCTTTTGTA
 GGATTtAATGGTGATTtTTCGAGCTTACAAGCACTTGAAACACCGATT
 TAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAATC
 ATAAAGACCAATTGGAGTATAATGAATCAGCTCCTTTTGAAGCAACAAC
 TATACTGCCTTGTAAACACAATCAGCGTCTTGGGGCTATGTTGATTATGT
 CaaaaATGGTGGGGAGTTAGAATTAGCACCGGAGAGTcCAAAAAGAATTA
 TTTTAGGAACTTTGTAGAATAAGGTTGAGGATAAAACAATTCTCTTTTG
 GAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGA
 TGGAAATAGGGATGAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTA
 AGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAA
 AGTAAGGTTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCA
 GAGTGATGGTCATTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAgATA
 AGGATGGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTAC
 ACACCAGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCA
 AGTAAGTACTAAGTCACCAATCTTCTTACGAGCTCAGTTTGATGaaa
 CTAATCGAACATTAAGCTTAGCCATGCCTAAGGGAAGTAGTTATGTTCT
 ATATATCGTCTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATA
 TGGAGATGAGACTTCTTACTATTATTTCCATATAGATCAAGAAGGTAAAG
 CGACACTTCTTAAACGGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGAC
 CCTAAGGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTCGAaC
 GGTAAAATTGTCTGACCTCTGAATAAGGCAGTAGTATCAGAGAAAGAAA
 ACGCTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAA
 GAACCTATGTTTATTCTAAAAAAGAAAAAGTAGTAAACAAGAATCTAGA
 AGAaATAATATTAGTTAAGCCGCAcACTACAGTTACTACTCaATCATTGT
 CTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCTCCTTCTACAAAC
 AATAATAGTAGTAGTAGCTAAAATCATATCACCTAAACATAATGGGGA
 TTCTGTTAACCATACC

SEQ ID NO. 4411

STRAIN JM9130013

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAA
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATCTGTT
 GAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT
 GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAG
 AGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAA
 GAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGT
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAG
 AGGTGAAGCCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTAAA
 ATAACAAAATTACAAGCCATAACCCAAAGAGGAAAGGGAATGTAGTAGC
 TATTATTGATACTGGCTTTGATATTAACCATGATATTTTCGTTTAGATA
 GCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAATTGAGGAA
 TTAAGCAAAACATAATATCACTTATGGGAAATGGGTAAACGATAAGAT
 TGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGCTGATATTG
 CAGCAGCTATGAAAGATGGTTATGGTTTCAGAAGCAAGAATATTTCGCAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCCAGCAAT
 CAATGGTCTTCTTTAGAAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAA
 TGCGTATTCAGATAAAATTGATTCCGACAAATTTGGTGAAGCATATGCT
 AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAG
 TATTGGAAAAACAGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAAAT
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCC
 GGAAATGAAGGCGCATTTGGTATGGATTATAGCAAACCATTATCAACTAA
 TCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA
 GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTCGTTGAAACA
 ACTATTGAAGGTAAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTT
 TGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA
 AAGACTTTGAAGGTAAAGGACTTTAAAGGTAAAGATTGCATTAAATTGAGCGT
 GGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAGG
 TGTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTTC
 TAATTCCTTACCGTGAATTACCTGTGGGGATTATTAGTAAAGTAGATGGC
 GAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTGA
 AGTAGTTGATAGCCAAGGTGGTAATCGTATGCTGGAACAATCAAGTTGGG
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT
 GAAATTTATCTTCAACCTATAATAATCAATACCAAACAATGTCTGGTAC
 AAGTATGGCTTCAACCATGTTGCAGGATTAAAGACAATGCTTCAAAGTC
 ATTTGGCTGAGAAATATAAAGGGaTGAATTTAGATTCTAAAAAATTGCTA
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
 AGAGGATAAGGCGTTTATTACACAGTCAGCAAGGTGCAGGTGTAGTTG
 ATGCTGAAAAAGCTATCCAAGCTCaATATTATATTACTGGAAACGATGGC
 AAAGCTAAATTAATCTCAAACGAATGGGAGATAAATTTGATATCACAGT
 TACAATTCAaAACTTGTAGAAGGTGTCAAAGAAaTGTATTATCAAGCTA
 ATGTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTaAACCAAA
 GCCTTGCTAGATACTAATTGGCAGAAAGTAAATCTTCTGATATAAAGAAAC
 ACAAGTTGCTATTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAGG
 AACAGATGGCAAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAAGAA
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTAA
 TGGTGATTTTGCGAACCTTACAAGCACTTGAACACCGATTATAAGACGC
 TTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAAGAC
 CAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTGC
 CTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATG
 GTGGGGAGTTAGAATTAGCAACCGAGAGTCCAAAAAGAATTATTTTAGGA
 ACTTTTGAGAAATAAGGTTGAGGATAAAACAATTCATCTTTTGAAAGAGA
 TGCAGCGAAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAATA
 GGGACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATT
 TCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAGTAAGGT
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG
 GTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTAGATAAGGATGGC
 AAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACCAGT
 AGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTA
 CTAAGTCACCAATCTTCTTTCAGAGCTCAGTTTGATGAAACTAATCGA
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCG
 TTTACAATTAGTTTTATCTCATGTTGTAAAGATGAAGAATATGGGGATG
 AGACTTCTTACCATATTTCCATATAGATCAAGAAGGTAAAGTGACACTT
 CCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGGC
 CTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCAaACGGTAAAT
 TGTCTGATCTCTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATA
 GTAATTTCTaACAGTTTCAAATATTTTGATAACTTGAAAAAAGAACCTAT
 GTTTATTTCTAAAAAAGAAAAAGTAGTAAACAAGAACTAGAGAAGAAATA
 TATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAA
 ATAACATAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATAG
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
 ACCATACC

PRETTY of: /biotmp/msa183564.2{*} May 13, 2003 03:28 ...

	1		50
msa183564.2{147_COH1}	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----
msa183564.2{147_2603}	gtggataaac	atcactcaaa	aaaggctatt
msa183564.2{147_JM9130013}	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----
Consensus	*****	*****	*****
	51		100
msa183564.2{147_COH1}	-----	-----	GAGGAGCAAG
msa183564.2{147_M732}	-----	-----	GAGGAGCAAG
msa183564.2{147_M781}	-----	-----	GAGGAGCAAG
msa183564.2{147_2603}	aactagatt	ttattaatgc	atagcaatca
msa183564.2{147_JM9130013}	-----	-----	agtgatgca
msa183564.2{147_18RS21}	-----	-----	GAGGAGCAAG
msa183564.2{147_090}	-----	-----	GAGGAGCAAG
msa183564.2{147_CJB110}	-----	-----	GAGGAGCAAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_A909}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_H36B}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_1169NT}	-----	-----	-----	-----	GAGGAGCAAG
Consensus	*****	*****	*****	*****	*****
101					
msa183564.2{147_COH1}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M732}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M781}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_2603}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_JM9130013}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_18RS21}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_090}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_CJB110}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_A909}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_H36B}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_1169NT}	AATTAAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
Consensus	*****	*****	*****	*****	*****
151					
msa183564.2{147_COH1}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_M732}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_M781}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_2603}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_JM9130013}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_18RS21}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_090}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_CJB110}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_A909}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_H36B}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_1169NT}	CCATCGCCAT	CGGTAACCTAC	TAATATGT	GAAAAAACAT	CTGTAAcAgC
Consensus	*****	*****	*****	*****	*****
201					
msa183564.2{147_COH1}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M732}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M781}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_2603}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_JM9130013}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_18RS21}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_090}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_CJB110}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_A909}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_H36B}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_1169NT}	TGCTTCTGCT	AGTAATACAG	cGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
Consensus	*****	*****	*****	*****	*****
251					
msa183564.2{147_COH1}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M732}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M781}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_2603}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_JM9130013}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_18RS21}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_090}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_CJB110}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_A909}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_H36B}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_1169NT}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
Consensus	*****	*****	*****	*****	*****
301					
msa183564.2{147_COH1}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M732}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M781}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_2603}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_JM9130013}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_18RS21}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_090}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_CJB110}	ACGTCTAATw	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_A909}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_H36B}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_1169NT}	ACGTCTAATa	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
Consensus	*****	*****	*****	*****	*****
351					
msa183564.2{147_COH1}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_M732}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_M781}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_2603}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_JM9130013}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_18RS21}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_090}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_CJB110}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_A909}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_H36B}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_1169NT}	GACAACCAAC	AATAAgGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
Consensus	*****	*****	*****	*****	*****
401					
msa183564.2{147_COH1}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAAGCAAG
msa183564.2{147_M732}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAAGCAAG
msa183564.2{147_M781}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAAGCAAG
msa183564.2{147_2603}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_JM9130013}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_18RS21}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_090}	TAGCACAGAA	AGTTCCCTCA	GCgTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_CJB110}	TAGCACAGAA	AGTTCCCTCA	GCgTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_A909}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_H36B}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAAGCAAG
msa183564.2{147_1169NT}	TAGCACAGAA	AGTTCCCTCA	GCaTATGAAG	AGGTGAAGcC	AaAAAAGCAAG
Consensus	*****	*****	**-*****	*****-*	*-*****
451					
msa183564.2{147_COH1}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M732}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M781}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_2603}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_JM9130013}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_18RS21}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_090}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_CJB110}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_A909}	TCATCaCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_H36B}	TCATCaCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_1169NT}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
Consensus	*****	*****	*****	*****	*-*****
501					
msa183564.2{147_COH1}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_M732}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_M781}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_2603}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_JM9130013}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_18RS21}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_090}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_CJB110}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_A909}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_H36B}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
msa183564.2{147_1169NT}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCTTTG
Consensus	*****	*****	*****	*****	*****
551					
msa183564.2{147_COH1}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_M732}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_M781}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_2603}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_JM9130013}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_18RS21}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_090}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_CJB110}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_A909}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_H36B}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
msa183564.2{147_1169NT}	ATATTAACCA	TGATATTTTT	CGTTTAGATA	GCCCCAAAAGA	TGATAAGCAC
Consensus	*****	*****	*****	*****	*****
601					
msa183564.2{147_COH1}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M732}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M781}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_2603}	AGCTTTAAAA	cTAaagCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_JM9130013}	AGCTTTAAAA	cTAaagCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_18RS21}	AGCTTTAAAA	cTAaagCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_090}	AGCTTTAAAA	cTAaagCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_CJB110}	AGCTTTAAAA	cTAaagCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_A909}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_H36B}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_1169NT}	AGCTTTAAAA	aTAaggCAGA	ATTcGAGGAA	TTAAAAGCAA	AACATAATAT
Consensus	*****	-****-****	***-*****	*****	*****
651					
msa183564.2{147_COH1}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M732}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M781}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_2603}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_JM9130013}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_18RS21}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_090}	CACTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_CJB110}	CACTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_A909}	CACTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_H36B}	CACTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_1169NT}	CACTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
Consensus	*****	*****	*****	*****	*****
701					
msa183564.2{147_COH1}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M732}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M781}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_2603}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_JM9130013}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_18RS21}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_090}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_CJB110}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_A909}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_H36B}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_1169NT}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
Consensus	*****	*****	*****	*****	*****
751					
msa183564.2{147_COH1}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M732}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M781}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_2603}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_JM9130013}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_18RS21}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_090}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_CJB110}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_A909}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_H36B}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_1169NT}	TATGGGTCAG	AAGCAAAGAA	TATTTcGCAT	GGTACACACG	TTGCTGGTAT
Consensus	*****	*****	*****	*****	*****
801					
msa183564.2{147_COH1}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_M732}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_M781}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_2603}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_JM9130013}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_18RS21}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_090}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_CJB110}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_A909}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_H36B}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
msa183564.2{147_1169NT}	TTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATgGTCTT	CTTTTAGAAG
Consensus	*****	*****	*****	*****	*****
851					
msa183564.2{147_COH1}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M732}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M781}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_2603}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_JM9130013}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_18RS21}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_090}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_CJB110}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_A909}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_H36B}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_1169NT}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
Consensus	*****	*****	*****	*****	*****
901					
msa183564.2{147_COH1}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M732}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M781}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_2603}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_JM9130013}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_18RS21}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_090}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_CJB110}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_A909}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_H36B}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_1169NT}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
Consensus	*****	*****	*****	*****	*****
951					
msa183564.2{147_COH1}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGCTGATT
msa183564.2{147_M732}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGCTGATT
msa183564.2{147_M781}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGCTGATT
msa183564.2{147_2603}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGCTGATT
msa183564.2{147_JM9130013}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGCTGATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_18RS21}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTgATT
msa183564.2{147_090}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTtGGAAAA	ACaGCaGATT
msa183564.2{147_CJB110}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTtGGAAAA	ACaGCaGATT
msa183564.2{147_A909}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTtGGAAAA	ACaGCaGATT
msa183564.2{147_H36B}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTtGGAAAA	ACaGCaGATT
msa183564.2{147_1169NT}	TAATCTAGGA	GCTAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTgATT
Consensus	*****	**_*****	*****	-_*_*****	**_*_*_*****
1001					
msa183564.2{147_COH1}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M732}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M781}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_2603}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_JM9130013}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_18RS21}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_090}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_CJB110}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_A909}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_H36B}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_1169NT}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
Consensus	*****	-*****	*****	*****	*****
1051					
msa183564.2{147_COH1}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_M732}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_M781}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_2603}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTtGG
msa183564.2{147_JM9130013}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTtGG
msa183564.2{147_18RS21}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTtGG
msa183564.2{147_090}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_CJB110}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_A909}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_H36B}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTtGG
msa183564.2{147_1169NT}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTtGG
Consensus	*****	*****	*****	*****	*_*_*****
1101					
msa183564.2{147_COH1}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M732}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M781}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_2603}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_JM9130013}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_18RS21}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_090}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_CJB110}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_A909}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_H36B}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_1169NT}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
Consensus	*****	*****_*	*****	*****	*****
1151					
msa183564.2{147_COH1}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M732}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M781}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_2603}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_JM9130013}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_18RS21}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_090}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_CJB110}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_A909}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_H36B}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_1169NT}	ATAGTCCAGC	TATTTCTGAA	GATACTTTGA	GTGTTGCTAG	CTATGAATCA
Consensus	*****	*****	*****	*****	*****
1201					
msa183564.2{147_COH1}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M732}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M781}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_2603}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_JM9130013}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_18RS21}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_090}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_CJB110}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_A909}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_H36B}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_1169NT}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
Consensus	*****	*****	*****	*****	*****
1251					
msa183564.2{147_COH1}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M732}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M781}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_2603}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_JM9130013}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_18RS21}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_090}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_CJB110}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_A909}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_H36B}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_1169NT}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
Consensus	*****	*****	*****	*****	*****
1301					
msa183564.2{147_COH1}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_M732}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_M781}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_2603}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_JM9130013}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_18RS21}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_090}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_CJB110}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_A909}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_H36B}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_1169NT}	ATGTGGTTTA	TGCCAATTAT	GGTGC.aAAA	AAAGACTTTG	AAGGTAAGGA
Consensus	*****	*****	*****-_*	*****-****	*****
1351					
msa183564.2{147_COH1}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M732}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M781}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_2603}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_JM9130013}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_18RS21}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_090}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_CJB110}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_A909}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_H36B}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_1169NT}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
Consensus	*****	*****	*****	*****	*****
1401					
msa183564.2{147_COH1}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M732}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M781}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_2603}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_JM9130013}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_18RS21}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_090}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_CJB110}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_A909}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_H36B}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_1169NT}	TGACTAAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
Consensus	*****	*****	*****	*****	*****
1451					
msa183564.2{147_COH1}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M732}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M781}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_2603}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_JM9130013}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_18RS21}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_090}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_CJB110}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_A909}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_H36B}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_1169NT}	TTTAACGATC	AAGAAAAACG	TGGAAATTTT	CTAATTCCTT	ACCGTGAATT
Consensus	*****	*****	*****	*****	*****
1501					
msa183564.2{147_COH1}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_M732}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_M781}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_2603}	ACCTGTGGGG	aTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_JM9130013}	ACCTGTGGGG	aTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_18RS21}	ACCTGTGGGG	aTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_090}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_CJB110}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_A909}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_H36B}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
msa183564.2{147_1169NT}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACTT
Consensus	*****	-*****	*****	*****	*****
1551					
msa183564.2{147_COH1}	CAAGTCAGTT	AACATTTAAC	CAGAGtTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M732}	CAAGTCAGTT	AACATTTAAC	CAGAGtTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M781}	CAAGTCAGTT	AACATTTAAC	CAGAGtTTTG	AAGTAGTTGA	TAGCCAAGGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_2603}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_JM9130013}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_18RS21}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_090}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_CJB110}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_A909}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_H36B}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_1169NT}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M732}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M781}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_2603}	GGtAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_JM9130013}	GGtAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_18RS21}	GGtAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_090}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_CJB110}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_A909}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_H36B}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_1169NT}	GGcAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
Consensus	**_*****	*****	*****	*****	*****
msa183564.2{147_COH1}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M732}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M781}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_2603}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_JM9130013}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_18RS21}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_090}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_CJB110}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_A909}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_H36B}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_1169NT}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	cGAAATTTAT	TCTTCAACCT
Consensus	*****	*****	*****	_*****	*****
msa183564.2{147_COH1}	ATAATAATCA	ATACtAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_M732}	ATAATAATCA	ATACtAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_M781}	ATAATAATCA	ATACtAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_2603}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_JM9130013}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_18RS21}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_090}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_CJB110}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_A909}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_H36B}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
msa183564.2{147_1169NT}	ATAATAATCA	ATACcAAACA	ATGTCTGGTA	CAAGTATGGC	TTCACCACAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_M732}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_M781}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_2603}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_JM9130013}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_18RS21}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_090}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_CJB110}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_A909}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_H36B}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
msa183564.2{147_1169NT}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTTGGCTG	AGAAATATAA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M732}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M781}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_2603}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_JM9130013}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_18RS21}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_090}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_CJB110}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_A909}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_H36B}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_1169NT}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT
msa183564.2{147_M732}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M781}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_2603}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_JM9130013}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_18RS21}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_090}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_CJB110}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_A909}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_H36B}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_1169NT}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M732}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M781}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_2603}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_JM9130013}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_18RS21}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_090}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_CJB110}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_A909}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_H36B}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_1169NT}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M732}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M781}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_2603}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_JM9130013}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_18RS21}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_090}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_CJB110}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_A909}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_H36B}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_1169NT}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
Consensus	*****	***-*****	*****	*****-****	*****
msa183564.2{147_COH1}	AACGAgagGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M732}	AACGAgagGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M781}	AACGAgagGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_2603}	AACGAatGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_JM9130013}	AACGAatGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_18RS21}	AACGAatGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_090}	AACGAgtGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_CJB110}	AACGAgtGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_A909}	AACGAgtGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_H36B}	AACGAgtGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_1169NT}	AACGAgtGGG	AGATAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
Consensus	*****-***	*****	*****	*****	*****
msa183564.2{147_COH1}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M732}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M781}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_2603}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_JM9130013}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_18RS21}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_090}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_CJB110}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_A909}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_H36B}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_1169NT}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M732}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M781}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_2603}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_JM9130013}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_18RS21}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_090}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_CJB110}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_A909}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_H36B}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_1169NT}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GGCAGAAAGT	AATTCCTCGT	GATAAAGAAA	CACAAGTTCG	ATTACTAATT

msa183564.2 {147_M732}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_M781}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_2603}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_JM9130013}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_18RS21}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_090}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_CJB110}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_A909}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_H36B}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
msa183564.2 {147_1169NT}	GGCAGAAAGT	AATTCTTCGT	GATAAAGAAA	CACAAGTTCCG	ATTTACTATT
Consensus	*****	*****	*****	*****	*****
msa183564.2 {147_COH1}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_M732}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_M781}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_2603}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_JM9130013}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_18RS21}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_090}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_CJB110}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_A909}	GATtCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_H36B}	GATtCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
msa183564.2 {147_1169NT}	GATgCTAGTC	AATTTAGTCA	GAAATTAAAA	GAACAGATGG	CAAATGGTTA
Consensus	***-*****	*****	*****	*****	*****
msa183564.2 {147_COH1}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_M732}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_M781}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_2603}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_JM9130013}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_18RS21}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_090}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_CJB110}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_A909}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_H36B}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
msa183564.2 {147_1169NT}	TTTCTTAGAA	GGTTTTGTAC	GTTTTAAAGA	AGCcAAGGAT	AGTAATCAGG
Consensus	*****	*****	*****	***-*****	*****
msa183564.2 {147_COH1}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_M732}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_M781}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_2603}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_JM9130013}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_18RS21}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_090}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_CJB110}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_A909}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_H36B}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAaCTTA
msa183564.2 {147_1169NT}	AGTTAATGAG	TATTCCTTTT	GTAGGATTTA	ATGGTGATTT	TGCGAgCTTA
Consensus	*****	*****	*****	*****	*****-****
msa183564.2 {147_COH1}	CAAGCACTTG	AAACACCGAT	TTATAAGACG	cTTTCTAAAG	GTAAGTTTCTA
msa183564.2 {147_M732}	CAAGCACTTG	AAACACCGAT	TTATAAGACG	cTTTCTAAAG	GTAAGTTTCTA
msa183564.2 {147_M781}	CAAGCACTTG	AAACACCGAT	TTATAAGACG	cTTTCTAAAG	GTAAGTTTCTA
msa183564.2 {147_2603}	CAAGCACTTG	AAACACCGAT	TTATAAGACG	cTTTCTAAAG	GTAAGTTTCTA
msa183564.2 {147_JM9130013}	CAAGCACTTG	AAACACCGAT	TTATAAGACG	cTTTCTAAAG	GTAAGTTTCTA
msa183564.2 {147_18RS21}	CAAGCACTTG	AAACACCGAT	TTATAAGACG	aTTTCTAAAG	GTAAGTTTCTA
msa1					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_COH1}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_M732}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_M781}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_2603}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_JM9130013}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_18RS21}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_090}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_CJB110}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_A909}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_H36B}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
msa183564.2{147_1169NT}	CAGCTCCTTT	TGAAAGCAAC	AACTATACTG	CCTTGTTAAC	ACAATCAGCG
Consensus	*****	*****	*****	*****	*****
2501					
msa183564.2{147_COH1}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M732}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M781}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_2603}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_JM9130013}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_18RS21}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_090}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_CJB110}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_A909}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_H36B}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_1169NT}	TCTTGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
Consensus	*****	*****	*****	*****	*****
2551					
msa183564.2{147_COH1}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_M732}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_M781}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_2603}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_JM9130013}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_18RS21}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_090}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_CJB110}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_A909}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_H36B}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
msa183564.2{147_1169NT}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACCTTTGAG	AATAAGGTTG
Consensus	*****	*****	*****	*****	*****
2601					
msa183564.2{147_COH1}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M732}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M781}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_2603}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_JM9130013}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_18RS21}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_090}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_CJB110}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_A909}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_H36B}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_1169NT}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
Consensus	*****	*****	*****	*****	*****
2651					
msa183564.2{147_COH1}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_M732}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_M781}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_2603}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_JM9130013}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_18RS21}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_090}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_CJB110}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_A909}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_H36B}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
msa183564.2{147_1169NT}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGAcGAAA	TCAC TCCCCA
Consensus	*****	*****	*****	*****	*****
2701					
msa183564.2{147_COH1}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M732}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M781}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_2603}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_JM9130013}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_18RS21}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_090}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_CJB110}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_A909}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_H36B}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_1169NT}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
Consensus	*****	*****	*****	*****	*****
2750					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_COH1}	2751	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	2800	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_M732}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_M781}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_2603}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_JM9130013}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_18RS21}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_090}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_CJB110}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_A909}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_H36B}	2751	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	2800	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_H36B}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	msa183564.2{147_1169NT}	AAAAATGGAAA	TGTTATTTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
	Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	2801	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	2850	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_M732}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_M781}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_2603}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_JM9130013}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_18RS21}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_090}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_CJB110}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_A909}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_H36B}	2801	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	2850	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_H36B}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	msa183564.2{147_1169NT}	AATTTCCATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
	Consensus	*****	*****	***-*****	*****	*****
msa183564.2{147_COH1}	2851	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	2900	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_M732}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_M781}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_2603}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_JM9130013}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_18RS21}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_090}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_CJB110}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_A909}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_H36B}	2851	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	2900	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_H36B}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	msa183564.2{147_1169NT}	tcTTCAGTGG	AGTGGTTTtag	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
	Consensus	--*****	*****	*****	*****	*****
msa183564.2{147_COH1}	2901	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	2950	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_M732}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_M781}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_2603}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_JM9130013}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_18RS21}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_090}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_CJB110}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_A909}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_H36B}	2901	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	2950	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_H36B}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	msa183564.2{147_1169NT}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
	Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	2951	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	3000	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_M732}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_M781}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_2603}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_JM9130013}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_18RS21}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_090}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_CJB110}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_A909}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_H36B}	2951	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	3000	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_H36B}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	msa183564.2{147_1169NT}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAATCTTCC
	Consensus	*****	*****	-*****	*****	*****
msa183564.2{147_COH1}	3001	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	3050	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_M732}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_M781}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_2603}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_JM9130013}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_18RS21}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_090}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_CJB110}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_A909}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
msa183564.2{147_H36B}	3001	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	3050	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_H36B}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	msa183564.2{147_1169NT}	TTcACgAGCT	CAGTTTgATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC
	Consensus	**--**--****	*****	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		3051				3100
msa183564.2	{147_COH1}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_M732}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_M781}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_2603}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_JM9130013}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_18RS21}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_090}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_CJB110}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_A909}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_H36B}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
msa183564.2	{147_1169NT}	CTAAGGaAAG	TAGTTATGTT	CCTAcATATC	GTtTACAATT	AGTTTATCT
Consensus		*****-***	*****	*****	*****	*****
		3101				3150
msa183564.2	{147_COH1}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_M732}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_M781}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_2603}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_JM9130013}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_18RS21}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_090}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_CJB110}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_A909}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_H36B}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
msa183564.2	{147_1169NT}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ACcATTATTT
Consensus		*****	*****	*****-***	*****	*****
		3151				3200
msa183564.2	{147_COH1}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_M732}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_M781}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_2603}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_JM9130013}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_18RS21}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_090}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_CJB110}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_A909}	CCATATAGAT	CgAGAAGGTA	AAGtGACACT	TCCTAAAACa	GTTAAGATAG
msa183564.2	{147_H36B}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACa	GTTAAGATAG
msa183564.2	{147_1169NT}	CCATATAGAT	CaAGAAGGTA	AAGcGACACT	TCCTAAAACg	GTTAAGATAG
Consensus		*****	*-*****	***-*****	*****-*	*****
		3201				3250
msa183564.2	{147_COH1}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_M732}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_M781}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_2603}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_JM9130013}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_18RS21}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_090}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_CJB110}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_A909}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGa	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_H36B}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGa	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_1169NT}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
Consensus		*****	*****-***	*****-*	*****	*****
		3251				3300
msa183564.2	{147_COH1}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_M732}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_M781}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_2603}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_JM9130013}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_18RS21}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_090}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_CJB110}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_A909}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_H36B}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_1169NT}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
Consensus		*****	*****-***	*****	*****-*	*****
		3301				3350
msa183564.2	{147_COH1}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_M732}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_M781}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_2603}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_JM9130013}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_18RS21}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_090}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_CJB110}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_A909}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_H36B}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_1169NT}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

Consensus	*****	*****	*****	*****	*****
	3351				3400
msa183564.2{147_COH1}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_M732}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_M781}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_2603}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_JM9130013}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_18RS21}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_090}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_CJB110}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_A909}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_H36B}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
msa183564.2{147_1169NT}	AATATTTTGA	TAACTTGAAG	AAAGAAcCTA	TGTTTATTTTC	TAAAgAAGgA
Consensus	*****	*****	*****	*****	*****
	3401				3450
msa183564.2{147_COH1}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCTCAaAC
msa183564.2{147_M732}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCTCAaAC
msa183564.2{147_M781}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCTCAaAC
msa183564.2{147_2603}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCgCAaAC
msa183564.2{147_JM9130013}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCgCAaAC
msa183564.2{147_18RS21}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCgCAaAC
msa183564.2{147_090}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCgCAaAC
msa183564.2{147_CJB110}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCgCAaAC
msa183564.2{147_A909}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	gcATTAGTTA	AGCCgCAaAC
msa183564.2{147_H36B}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	gcATTAGTTA	AGCCgCAaAC
msa183564.2{147_1169NT}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCgCAaAC
Consensus	*****	*****	*****	*****	*****
	3451				3500
msa183564.2{147_COH1}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M732}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M781}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_2603}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_JM9130013}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_18RS21}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_090}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_CJB110}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_A909}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTcAA	TCAGGAAATG
msa183564.2{147_H36B}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTcAA	TCAGGAAATG
msa183564.2{147_1169NT}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
Consensus	*****	*****	*****	*****	*****
	3501				3550
msa183564.2{147_COH1}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_M732}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_M781}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_2603}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_JM9130013}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_18RS21}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_090}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_CJB110}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_A909}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_H36B}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_1169NT}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGtAGAGT	AGCTAAaATC
Consensus	*****	*****	*****	*****	*****
	3551				3600
msa183564.2{147_COH1}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_M732}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_M781}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_2603}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_JM9130013}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_18RS21}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_090}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_CJB110}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_A909}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_H36B}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
msa183564.2{147_1169NT}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	~~~~~
Consensus	*****	*****	*****	*****	*****
	3601				3650
msa183564.2{147_COH1}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_M732}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_M781}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_2603}	atcagataga	gcaacgaatg	gtctatttgt	tggtactttg	gcattgttat
msa183564.2{147_JM9130013}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_18RS21}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_090}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_CJB110}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_A909}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa183564.2{147_H36B}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3651				3700
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	ctagtttact	tctttatttg	aaacccaaaa	agactaaaaa	taatagtaaa
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 4412**STRAIN 2603**

VDKHHSKKA I L K L T L I T T S I L L M H S N Q V N A E E Q E L K N Q E Q S P V I A N V A Q Q P S P S V T T N T V
E K T S V T A A S A N T A K E M G D T S V K N D K T E D E L L E E L S K N L D T S N L G A D L E E E Y P S K P E T T N
N K E S N V V T N A S T A I A Q K V P S A Y E E V K P E S K S S L A V L D T S K I T K L Q A I T Q R G K G N V V A I I D
T G F D I N H D I F R L D S P K D D K H S F K T K T E F E E L K A K H N I T Y G K W V N D K I V F A H N Y A N N T E T V
A D I A A M K D G Y G S E A K N I S H G T H V A G I F V G N S K R P A I N G L L L E G A A P N A Q V L L M R I P D K I
D S D K F G E A Y A K A I T D A V N L G A K T I N M S I G K T A D S L I A L N D K V K L A L K L A S E K G V A V V V A A
G N E G A F G M D Y S K P L S T N P D Y G T V N S P A I S E D T L S V A S Y E S L K T I S E V V E T T I E G K L V K L P
I V T S K P F D K G K A Y D V V Y A N Y G A K K D F E G K D F G K I A L I E R G G G L D F M T K I T H A T N A G V V G
I V I F N D Q E K R G N F L I P Y R E L P V G I I S K V D G E R I K N T S S Q L T F N Q S F E V V D S Q G G N R M L E Q
S S W G V T A E G A I K P D V T A S G F E I Y S S T Y N N Q Y Q T M S G T S M A S P H V A G L M T M L Q S H L A E K Y K
G M N L D S K K L L E L S K N I L M S S A T A L Y S E E D K A F Y S P R Q Q G A G V V D A E K A I Q A Q Y Y I T G N D G
K A K I N L K R M G D K F D I T V T I H K L V E G V K E L Y Y Q A N V A T E Q V N K G K F A L K P Q A L L D T N W Q K V
I L R D K E T Q V R F T I D A S Q F S Q K L K E Q M A N G Y F L E G F V R F K E A K D S N Q E L M S I P F V G F N G D F
A N L Q A L E T P I Y K T L S K G S F Y Y K P N D T T H K D Q L E Y N E S A P F E S N N Y T A L L T Q S A S W G Y V D Y
V K N G G E L E L A P E S P K R I I L G T F E N K V E D K T I H L L E R D A A N N P Y F A I S P N K D G N R D E I T P Q
A T F L R N V K D I S A Q V L D Q N G N V I W Q S K V L P S Y R K N F H N N P K Q S D G H Y R M D A L Q W S G L D K D G
K V V A D G F Y T Y R L R Y T P V A E G A N S Q E S D F K V Q V S T K S P N L P S R A Q F D E T N R T L S L A M P K E S
S Y V P T Y R L Q L V L S H V V K D E E Y G D E T S Y H Y F H I D Q E G K V T L P K T V K I G E S E V A V D P K A L T L
V V E D K A G N F A T V K L S D L L N K A V V S E K E N A I V I S N S F K Y F D N L K K E P M F I S K K E K V V N K N L
E E I I L V K P Q T T V T T Q S L S K E I T K S G N E K V L T S T N N N S S R V A K I I S P K H N G D S V N H T L P S T
S D R A T N G L F V G T L A L L S S L L L Y L K P K K T K N N S K

SEQ ID NO. 4413**STRAIN A909**

E E Q E L K N Q E Q S P V I A N V A Q Q P S P S V T T N T V E K T S V T S A S A N T A K E M G D T S V K N D K T E D E
L L E E L S K N L D T S N L G A D L E E E Y P S K P E T T N N K E S N V V T N A S T A I A Q K V P S A Y E E V K P E S K
S S L A V L D T S K I T K L Q A I T Q R G K G N V V A I I D T G F D I N H D I F R L D S P K D D K H S F K T K A E F E E
L K A K H N I T Y G K W V N D K I V F A H N Y A N N T E T V A D I A A M K D G Y G S E A K N I S H G T H V A G I F V G
N S K R P A I N G L L L E G A A P N A Q V L L M R I P D K I D S D K F G E A Y A K A I T D A V N L G A K T I N M S L G K
T A D S L I A L N D K V K L A L K L A S E K G V A V V V A A G N E G A F G M D Y S K P L S T N P D Y G T V N S P A I S E
D T L S V A S Y E S L K T I S E V V E T T I E G K L V K L P I V T S K P F D K G K A Y D V V Y A N Y G A K K R L . R . G
L . R . D C I N . A W W W T . F Y D . N H S C Y K R C C W Y R Y F . R S R K T W K F S N S L P . I T C G G Y . . S R W
R A Y K K Y F K S V N I . P E F . S S . . P R W Q S Y A G T I K L G R D S . R S N Q A . C N S F W L . N L F F N L . . S
I P N N V W Y K Y G F T T C C R I N D N A S K S F G . E I . R D E F R F . K I A R I V . K H P H E L S N S I I . . R G .
G V L F T S A R C R C S . C . K S Y P S S I L C Y W K R W O S . N . S O T S G R . I . Y H S Y N S . T C R R C Q R I V
L S S . C S N R T S K . R . I C P . T T S L A R Y . L A E S N S S . . R N T S S I Y Y . F . S I . S E I K R T D G K W L
F L R F C T F . R S Q G . . S G V N E Y S F C R I . W . F C E L T S T . N T D L . D A F . R . F L L . T K . Y N S . R
P I G V Q . I S S F . K Q Q L Y C L V N T I S V L G L C . L C Q K W G V R I S T G E S K K N Y F R N F . E . G . G . N
N S S F G K R C S E . S I F C H F S K . R W K . G . N H S P G N F L K K C . G Y F C S S S R S K W K C Y L A K . G F T I
L S . K F P . . S K A K . W S L S Y G C P S V E W F R . G W Q S C S R W F L Y L S F T L H T S S R R S K . S G V R L . S
S S K Y . V T K S S F T S S V . . N . S N I K L S H A . G K . L C S Y I S S T I S F I S C C K R . R I W R . D F L P L F
P Y R S R R . S D T S . N S . D R R E . G C S R P . D L D T C C G R . S W . F R N G K I V . P L E . G S S I R E R K R Y
S N F . Q F Q I F . . L E K R T Y V Y F . R R K S S Q E S R R N S I S . A A N Y S Y Y S I I V . R N N S I R K . E S P
H F Y K Q . . . Q S S . D H I T . T . R G F C . P Y

SEQ ID NO. 4414**STRAIN H36B**

E E Q E L K N Q E Q S P V I A N V A Q Q P S P S V T T N T V E K T S V T S A S A N T A K E M G D T S V K N D K T E D E
L L E E L S K N L D T S N L G A D L E E E Y P S K P E T T N N K E S N V V T N A S T A I A Q K V P S A Y E E V K P E S K
S S L A V L D T S K I T K L Q A I T Q R G K G N V V A I I D T G F D I N H D I F R L D S P K D D K H S F K T K A E F E E
L K A K H N I T Y G K W V N D K I V F A H N Y A N N T E T V A D I A A M K D G Y G S E A K N I S H G T H V A G I F V G
N S K R P A I N G L L L E G A A P N A Q V L L M R I P D K I D S D K F G E A Y A K A I T D A V N L G A K T I N M S L G K
T A D S L I A L N D K V K L A L K L A S E K G V A V V V A A G N E G A F G M D Y S K P L S T N P D Y G T V N S P A I S E
D T L S V A S Y E S L K T I S E V V E T T I E G K L V K L P I V T S K P F D K G K A Y D V V Y A N Y G A K K D F E G K D
F K G K I A L I E R G G G L D F M T K I T H A T N A G V V G I V I F N D Q E K R G N F L I P Y R E L P V G V I S K V D G
E R I K N T S S Q L T F N Q S F E V V D S Q G G N R M L E Q S S W G V T A E G A I K P D V T A S G F E I Y S S T Y N N Q
Y Q T M S G T S M A S P H V A G L M T M L Q S H L A E K Y K G M N L D S K K L L E L S K N I L M S S A T A L Y S E E D K
A F Y S P R Q Q G A G V V D A E K A I Q A Q Y Y V T G N D G K A K I N L K R V G D K F D I T V T I H K L V E G V K E L Y
Y Q A N V A T E Q V N K G K F A L K P Q A L L D T N W Q K V I L R D K E T Q V R F T I D S S Q F S Q K L K E Q M A N G Y
F L E G F V R F K E A K D S N Q E L M S I P F V G F N G D F A N L Q A L E T P I Y K T L S K G S F Y Y K P N D T T H K D
Q L E Y N E S A P F E S N N Y T A L L T Q S A S W G Y V D Y V K N G G E L E L A P E S P K R I I L G T F E N K V E D K T
I H L L E R D A A N N P Y F A I S P N K D G N R D E I T P Q A T F L R N V K D I S A Q V L D Q N G N V I W Q S K V L P S
Y R K N F H N N P K Q S D G H Y R M D A L Q W S G L D K D G K V V A D G F Y T Y R L R Y T P V A E G A N S Q E S D F K V
Q V S T K S P N L P S R A Q F D E T N R T L S L A M P K E S S Y V P T Y R L Q L V L S H V V K D E E Y G D E T S Y H Y F

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

HIDQEGKVTLPKTVKIGESEVAVDPKTLTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNNFKYFDNLKKEPMFISKKEKVVNKNLEELALVKPQTTVTTQSLSKETQSGNEKVL
TSTNNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4415**STRAIN 18RS21**

EEQELKNQEQQSPVIANVAQQPSPSVTTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKTEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKI THATNAGVVGIVIFNDQEKGRNFLIPYRELPGVIGISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTABGAIKPDVTASGFEIYSSTYNNQ
YQTMGSMTSMASPHVAGLMTMLQSHLAEKYKGMNLDSSKLLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAAEKAIQAQYYITGNDGKAKINLKRMDGKFDITVTIHKLVEGVKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTSKGSFYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPKNKDGNRDEITPQATFLRNVDKISAOQLDQNGNVIWQSKVLPS
YRKNFHNPNKQSDGHYRMDALQWGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKESSYVPTYRLQLVLSHVVKDEEYGDETSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNSFKYFDNLKKEPMFISKKEKVVNKNLEELILVKPQTTVTTQSLSKETKSGNEKVL
TSTNNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4416**STRAIN M732**

EEQELKNQEQQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKSES
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG
NSKRPAINSLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIIIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQVLLVSLFLTICKNVEIF.FLTVNYLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHMLQD..QCFKVIWLRNIKG.I.ILKNC.NCLKTSS.AQQQHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPNHNKPC.ILIGRK.FFVIKKHKFDLLMLVNLVRN.KNRWQMI
S.KVLYVLKKPRIVIRS..VFLD.DLMVILRTYKHLKHRFIRFLKVVSTINQMIQLIKT
NWSTMNQLLKKATTILPC.HNQRGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
FIFWKEMQRIIHILPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIVWMLFSGVV.IRMAKL.QMVFIILAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELSSLMKLIH.A.PCLRKVMFLHIVYN.FYLM.LKMKNMGMRLLTIIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YORKKTL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4417**STRAIN COH1**

EEQELKNQEQQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKSES
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG
NSKRPAINSLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIIIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQVLLVSLFLTICKNVEIF.FLTVNYLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHMLQD..QCFKVIWLRNIKG.I.ILKNC.NCLKTSS.AQQQHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPNHNKPC.ILIGRK.FFVIKKHKFDLLMLVNLVRN.KNRWQMI
S.KVLYVLKKPRIVIRS..VFLD.DLMVILRTYKHLKHRFIRFLKVVSTINQMIQLIKT
NWSTMNQLLKKATTILPC.HNQRGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
FIFWKEMQRIIHILPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIVWMLFSGVV.IRMAKL.QMVFIILAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELSSLMKLIH.A.PCLRKVMFLHIVYN.FYLM.LKMKNMGMRLLTIIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YORKKTL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4418**STRAIN M781**

EEQELKNQEQQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKSES
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG
NSKRPAINSLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIIIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQVLLVSLFLTICKNVEIF.FLTVNYLWGLLVK.MA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SV.KILQVS.HLTRVLK.LIAKVAIVCWNNOVGA.QLKEQSSLM.QLLALKFIFLOPIIIN
TKQCLVQVWLHMLQD..QCFKVIWLRNIGK.I.ILKNC.NCLKTSS.AQQQHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPNHNKPC.ILIGRK.FFVIKKHKFDLLMLVNLVRN.KNRWQMVI
S.KVLYVLKKPRIVIRS..VFLD.DLMVILRTYKHLKHRFIRRFLKVSTINQMIQLIKT
NWSTMNQLLLKATTILPC.HNQLGAMLIMSKMVG.S.N.HRRVQKELF.ELLRIRLRKQ
FIFWKEMQRIIHLPLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISII IQSKVMVIVWMLFSGVV.IRMAKL.QMVFLIAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELKSLMKLIEH.A.PCLRKVVMLHIVYN.FYLM.L.KMKNMGMRLLTIIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKT.
.FLTVSNILIT.RKNLCFLKKEK..TRI.KK.H.LSLKLQLLNHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4419**STRAIN JM9130013**

EEQELKNQEQSPVIANVAQQPSPSVTTINTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKTEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVVISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGAIKPDVTASGFEIYSSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAKEYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVVDAAEKAIQAQYYITGNDGKAKINLKRMDGKFDITVTIHKLVEGVKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTL SKGSFYYPKNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGT FENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDALQWSGLDKDGKVADGFTYRRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKESYVPTYRLQLVL SHVVKDEEYGDETS YHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALT LVVEDKAGNFATVKLSDDL NKA VVSEKENAI
VISNSFKYFDNLKKEPMFISKEGKVNNKNLEEII LVK PQT TVTTQSL SKEITKSGNEKVL
TSTNNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4420**STRAIN 090**

EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVVISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGAIKPDVTASGFEIYSSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAKEYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVVDAAEKAIQAQYYVTGNDGKAKINLKRVDGKFDITVTIHKLVEGVKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTL SKGSFYYPKNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGT FENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDAFQWSGLDKDGKVADGFTYRRLRYTPVAEGANSQESDFKV
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVL SHVVKDEEYGDETS YHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALT LVVEDKAGNFATVKLSDDL NKA VVSEKENAI
VISNSFKYFDNLKKEPMFISKEGKVNNKNLEEII LVK PQT TVTTQSL SKEITKSGNEKVL
TSTNNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4421**STRAIN CJB110**

EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVVISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGAIKPDVTASGFEIYSSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAKEYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVVDAAEKAIQAQYYVTGNDGKAKINLKRVDGKFDITVTIHKLVEGVKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTL SKGSFYYPKNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGT FENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDAFQWSGLDKDGKVADGFTYRRLRYTPVAEGANSQESDFKV
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVL SHVVKDEEYGDETS YHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALT LVVEDKAGNFATVKLSDDL NKA VVSEKENAI
VISNSFKYFDNLKKEPMFISKEGKVNNKNLEEII LVK PQT TVTTQSL SKEITKSGNEKVL
TSTNNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4422

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

STRAIN 1169NT					
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTAKEMGDTSVKNDKTEDE					
LLEELSKNLDTSNMGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPKSK					
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFIDINHDI FRDLSPKDDKHSFKNAEFEE					
LKAKHNITYGKWNVDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG					
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK					
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE					
DTLSVASYESLKTISEVVETITIEGKLVKLPVTSKPPDKGKAYDVVYANYGAKKDFEGKD					
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVVISKVDG					
ERIKNTSSQLTFNQRFVVDSSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSYNNQ					
YQTMSTSMASPHVAGLMTMLQSHLAKEYKGMNLDKSKLLELSKNILMSSATALYSEEDK					
AFYSPRQQGAGVVDKAIQAQYYVTGNDGKAKINLKRVDGDKFDITVTIHKLVEGVKELY					
YQANVATEQVNGKGFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY					
FLEGFVRFKEAKDSNQELMSIPFVGFGNDFASLQALETPITYKLSKGSFYYPKNDTTHKD					
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGEELAPESPKRIILGTFENKVEDKT					
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS					
YRKNFHNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV					
QVSTKSPNLPRAQFDETNRSLAMPKGSYVPIYRLQLVLSHVVKDEEYGDSETSYYF					
HIDQEGKATLPKTVKIGESEVAVDPKALTLLVEDKAGNFATVKLSDDLNKAVVSEKENAI					
VISNSFKYFDNLKKEPMFISKKEKVVNKNLEELILVKPHTTVTQSLSKETKSGNEKVL					
TSTNNSSRVAKIISPKNHNGDSVNHT					
PRETTY of: /biotmp/msa209368.2{*} February 10, 2003 02:09 ..					
1 50					
msa209368.2{147_COH1}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_M732}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_M781}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_18RS21}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_2603}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_JM9130013}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_090}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_CJB110}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_1169NT}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_H36B}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
msa209368.2{147_A909}	-----	-----	-----	EEQELKNQEQ	SPVIANVAQQ
Consensus	*****	*****	*****	*****	*****
51 100					
msa209368.2{147_COH1}	PSPSVTTNtV	EKTSVTaASA	SNTvKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M732}	PSPSVTTNtV	EKTSVTaASA	SNTvKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M781}	PSPSVTTNtV	EKTSVTaASA	SNTvKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_18RS21}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_2603}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_JM9130013}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_090}	PSPSVTTNtV	EKTSVTaASA	SNTvKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_CJB110}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_1169NT}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_H36B}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_A909}	PSPSVTTNtV	EKTSVTaASA	SNTaKEMGDT	SVKNDKTEDE	LLEELSKNLD
Consensus	*****-*	*****-***	***-*****	*****	*****
101 150					
msa209368.2{147_COH1}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKseSK
msa209368.2{147_M732}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKseSK
msa209368.2{147_M781}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKseSK
msa209368.2{147_18RS21}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_2603}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_JM9130013}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_090}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_CJB110}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_1169NT}	TSNmGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpkSK
msa209368.2{147_H36B}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_A909}	TSNlGADLEE	EYPSKPETT	NKESNVVTNA	STAIAQKVPS	AYEEVKpeSK
Consensus	***-*****	*****	*****	*****	*****-***
151 200					
msa209368.2{147_COH1}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_M732}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_M781}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_18RS21}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_2603}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_JM9130013}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_090}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_CJB110}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_1169NT}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_H36B}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
msa209368.2{147_A909}	SSLAVLDTSK	ITKLQAtQR	GKGNVVAIID	TGFDINHDI	RLDSPKDDKH
Consensus	*****-****	*****-***	*****	*****	*****
201 250					
msa209368.2{147_COH1}	SFKtKaEFEE	LKAKHNITYG	KWNVDKIVFA	HNYANNTETV	ADIAAAMKDG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_M732}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_M781}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_18RS21}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_2603}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_JM9130013}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_090}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_CJB110}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_1169NT}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_H36B}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_A909}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
Consensus	***-*-****	*****	*****	*****	*****
251					
msa209368.2{147_COH1}	YGSEAKNIH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M732}	YGSEAKNIH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M781}	YGSEAKNIH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_18RS21}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_2603}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_JM9130013}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_090}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_CJB110}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_1169NT}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_H36B}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_A909}	YGSEAKNIsh	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
Consensus	*****-*	*****	*****-*	*****	*****
301					
msa209368.2{147_COH1}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M732}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M781}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_18RS21}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSiGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_2603}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSiGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_JM9130013}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSiGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_090}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_CJB110}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_1169NT}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSiGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_H36B}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_A909}	DSDKFGEAYA	KAIIdAVNLG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
Consensus	*****	***-*****	*****-*	*****	*****
351					
msa209368.2{147_COH1}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_M732}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_M781}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_18RS21}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_2603}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_JM9130013}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_090}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_CJB110}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_1169NT}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_H36B}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
msa209368.2{147_A909}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPDY	GTVNSPAISE	DTLSVASYES
Consensus	*****	*****	*****	*****	*****
401					
msa209368.2{147_COH1}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M732}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M781}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_18RS21}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_2603}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_JM9130013}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_090}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_CJB110}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_1169NT}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_H36B}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_A909}	LKTISEVVET	TIEGKLVKLP	IVTSKPFDDG	KAYDVVYANY	GAKKrl.r.g
Consensus	*****	*****	*****	*****	*****
451					
msa209368.2{147_COH1}	lkvrlh.lsv	vvdlii.lks	lmlqmqvllv	slfltikknv	eiF.fltvny
msa209368.2{147_M732}	lkvrlh.lsv	vvdlii.lks	lmlqmqvllv	slfltikknv	eiF.fltvny
msa209368.2{147_M781}	lkvrlh.lsv	vvdlii.lks	lmlqmqvllv	slfltikknv	eiF.fltvny
msa209368.2{147_18RS21}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_2603}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_JM9130013}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_090}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_CJB110}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_1169NT}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_H36B}	fkkgkialier	gggldfmtki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_A909}	l.r.dcin.a	wwwt.fyd.n	hscykcrcw	yryf.rsrkt	wkFsnslp.i
Consensus	-----	-----	-----	-----	-----
501					
550					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_COH1}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M732}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M781}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_18RS21}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_2603}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_JM9130013}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_090}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_CJB110}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_1169NT}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_H36B}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttega
msa209368.2{147_A909}	tcGgy..srw	rayKkyfksv	ni.pef.ss.	.prwqsyagt	iklgrds.rs
Consensus	---*-----	---*-----	-----	-----	-----
551					600
msa209368.2{147_COH1}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnik
msa209368.2{147_M732}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnik
msa209368.2{147_M781}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnik
msa209368.2{147_18RS21}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_2603}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_JM9130013}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_090}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_CJB110}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_1169NT}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_H36B}	ikpdvtasgf	eiysstynnq	yqtmstgtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_A909}	nqa.cnsfwl	.nlffnl..s	ipnnvwykyg	fttccrindn	asksfg.ei.
Consensus	-----	-----	-----	-----	-----
601					650
msa209368.2{147_COH1}	g.i.ilknk.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M732}	g.i.ilknk.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M781}	g.i.ilknk.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_18RS21}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_2603}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_JM9130013}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_090}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_CJB110}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_1169NT}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_H36B}	gmnlaskkll	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_A909}	rdefrf.kia	riv.khphel	snsii..rg.	gvlfttsarc	rsc.c.Ksyp
Consensus	-----	-----	-----	-----	-----*
651					700
msa209368.2{147_COH1}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M732}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M781}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_18RS21}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_2603}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_JM9130013}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_090}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_CJB110}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_1169NT}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_H36B}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkvkely	yqanvateqv
msa209368.2{147_A909}	ssilcywkrw	qs.n.sqtsg	r.i.yhsyns	.tcrregriv	lss.csnrts
Consensus	-----	-----	-----	-----	-----
701					750
msa209368.2{147_COH1}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M732}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M781}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_18RS21}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_2603}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_JM9130013}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_090}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_CJB110}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_1169NT}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_H36B}	nkqkfalkpq	alldtnwqkv	ilrldketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_A909}	k.r.icp.tt	slary.laes	nss..rntss	iyy.f.si.s	eiKrtgkwl
Consensus	-----	-----	-----	-----	---*-----
751					800
msa209368.2{147_COH1}	s.kvlyvlkk	privirs..v	flldlmvil	rtykhkhkrf	irrfkvkst
msa209368.2{147_M732}	s.kvlyvlkk	privirs..v	flldlmvil	rtykhkhkrf	irrfkvkst
msa209368.2{147_M781}	s.kvlyvlkk	privirs..v	flldlmvil	rtykhkhkrf	irrfkvkst
msa209368.2{147_18RS21}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_2603}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_JM9130013}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_090}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_CJB110}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_1169NT}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_H36B}	flegfvrke	akdsngelms	ipfvfngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_A909}	flrrfctf.r	sqq..sgvne	ysfcric.w.f	celtst.ntd	l.daf.r.fl
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	801				850
msa209368.2{147_COH1}	inqmiqlikt	nwstmnql11	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M732}	inqmiqlikt	nwstmnql11	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M781}	inqmiqlikt	nwstmnql11	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_18RS21}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_2603}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_JM9130013}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_090}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_CJB110}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_1169NT}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_H36B}	ykpnndtthkd	qleynesapf	esnnytal1t	qsaswgyvdy	vknggelela
msa209368.2{147_A909}	l.tk.yns.r	pigvq.issf	.kqqlyclvn	tisvlglc.l	cqkwwgvris
Consensus	-----	-----	-----	-----	-----
	851				900
msa209368.2{147_COH1}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M732}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M781}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_18RS21}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_2603}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_JM9130013}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_090}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_CJB110}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_1169NT}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_H36B}	pespKriilg	tfenkvedkt	ihllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_A909}	tgesKknyfr	nf.e.g.g.n	nssfgkrcse	.sifchfsk.	rwk.g.nhsp
Consensus	-----	-----	-----	-----	-----
	901				950
msa209368.2{147_COH1}	qls.emlriif	llkf.ikmem	lfgkvrifyhl	ivkisiiiqs	kvmviiwml
msa209368.2{147_M732}	qls.emlriif	llkf.ikmem	lfgkvrifyhl	ivkisiiiqs	kvmviiwml
msa209368.2{147_M781}	qls.emlriif	llkf.ikmem	lfgkvrifyhl	ivkisiiiqs	kvmviiwml
msa209368.2{147_18RS21}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_2603}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_JM9130013}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_090}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_CJB110}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_1169NT}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_H36B}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_A909}	gnflkkc.gy	fcsssrskwk	cylak.gfti	ls.kfp..sk	ak.wslsygc
Consensus	-----	-----	-----	-----	-----
	951				1000
msa209368.2{147_COH1}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M732}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M781}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_18RS21}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_2603}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_JM9130013}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_090}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_CJB110}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_1169NT}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_H36B}	lqwsqldkdg	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnlp
msa209368.2{147_A909}	psvewfr.gw	qscsrwFlyl	sftlhtserr	sk.sgvr1.s	ssky.vtkss
Consensus	-----	-----	-----	-----	-----
	1001				1050
msa209368.2{147_COH1}	helslmk1ie	h.a.pclrkv	vmflhivyn.	fylml.Kmkn	mgmrlltiis
msa209368.2{147_M732}	helslmk1ie	h.a.pclrkv	vmflhivyn.	fylml.Kmkn	mgmrlltiis
msa209368.2{147_M781}	helslmk1ie	h.a.pclrkv	vmflhivyn.	fylml.Kmkn	mgmrlltiis
msa209368.2{147_18RS21}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_2603}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_JM9130013}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_090}	llaqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_CJB110}	llaqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_1169NT}	sraqfdetnr	tlslampkes	syvpiyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_H36B}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetasyhyf
msa209368.2{147_A909}	ftssv..n.s	niklsha.gk	.lcsyissti	sfisccKr.r	iwr.dflplf
Consensus	-----	-----	-----	-----	-----
	1051				1100
msa209368.2{147_COH1}	i.ikkvk.hf	lkrlr.ervr	lr.tlrrp.hl	lwkiklvilq	r.nclts.ir
msa209368.2{147_M732}	i.ikkvk.hf	lkrlr.ervr	lr.tlrrp.hl	lwkiklvilq	r.nclts.ir
msa209368.2{147_M781}	i.ikkvk.hf	lkrlr.ervr	lr.tlrrp.hl	lwkiklvilq	r.nclts.ir
msa209368.2{147_18RS21}	hidqegkv1l	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_2603}	hidqegkv1l	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_JM9130013}	hidqegkv1l	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_090}	hidqegkv1l	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_CJB110}	hidqegkv1l	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_1169NT}	hidqegkat1	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_H36B}	hidqegkv1l	pktvkigese	vavdpkalt1	vvedkagnfa	tvklsl1lnk
msa209368.2{147_A909}	pyrsrr.sdt	s.ns.drre.	gcsrp.dldt	ccgr.sw.fr	ngkiv.ple.
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	1101			1150
msa209368.2{147_COH1}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl			
msa209368.2{147_M732}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl			
msa209368.2{147_M781}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl			
msa209368.2{147_18RS21}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqt			
msa209368.2{147_2603}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqt			
msa209368.2{147_JM9130013}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqt			
msa209368.2{147_090}	avvsekenai visnsfkyfd nlkKesmfis kegKvvknkl eeitlvkpqt			
msa209368.2{147_CJB110}	avvsekenai visnsfkyfd nlkKesmfis kegKvvknkl eeitlvkpqt			
msa209368.2{147_1169NT}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpht			
msa209368.2{147_H36B}	avvsekenai visnnfkyfd nlkKepmfis kegKvvknkl eeialvlpqt			
msa209368.2{147_A909}	gssirerkry snf.qfqif. .leKrtvyvf .rrKsskqes rrnsis.aan			
Consensus	-----	-----	-----	-----
	1151			1200
msa209368.2{147_COH1}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlntg illti-----			
msa209368.2{147_M732}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlntg illti-----			
msa209368.2{147_M781}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlntg illti-----			
msa209368.2{147_18RS21}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT----			
msa209368.2{147_2603}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhTlpst			
msa209368.2{147_JM9130013}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT----			
msa209368.2{147_090}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT----			
msa209368.2{147_CJB110}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT----			
msa209368.2{147_1169NT}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT----			
msa209368.2{147_H36B}	tvttqslske itqsgnekvl tstnnssrv akiispkhng dsvnhT----			
msa209368.2{147_A909}	ysyysiiv.r nnsirk.esp hfykq...qs s.dhit.t.r gfc.py----			
Consensus	-----	-----	-----	-----
	1201		1233	
msa209368.2{147_COH1}	-----	-----	---	
msa209368.2{147_M732}	-----	-----	---	
msa209368.2{147_M781}	-----	-----	---	
msa209368.2{147_18RS21}	-----	-----	---	
msa209368.2{147_2603}	sdratnglfv gtlallssll lylkpkktkn nsk			
msa209368.2{147_JM9130013}	-----	-----	---	
msa209368.2{147_090}	-----	-----	---	
msa209368.2{147_CJB110}	-----	-----	---	
msa209368.2{147_1169NT}	-----	-----	---	
msa209368.2{147_H36B}	-----	-----	---	
msa209368.2{147_A909}	-----	-----	---	
Consensus	*****	*****	***	

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

SEQ ID NO. 4501

STRAIN 2603

ATGAAAAAGATTAGAAAAAGTTTAGGACTTCTACTATGTTGCTTTTTAGGATTGGTACAA
 TTAGCGTTTTTTTCGGTAGCCAGTGTAATGCTGATACCCCTAATCAACTAACAATCACA
 CAGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGGACTGTG
 ACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATAGCGAATTGAACCAGAAG
 TATAAGAGTATCTTGACTTCTCCTACTGATACTAATGGTCAGACAAAGATAGCACTCCCA
 AATGGTTCGTACTTTGGTCGTGCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCT
 TTTTATATTGAATTACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGA
 AAAGTTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGATAAAGAAA
 AGGCTATCCGGAGTAATATTTGTATTATACGATAACCAGAATCAGCCAGTTCGCTTTAAA
 AATGGACGATTTACGACCGATCAAGATGGGATTACTTCATTAGTAAGTATGATAAGGGA
 GAAATTGAGGTTGAAGGTTTATTACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTA
 ACTGGTTACCGTATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAG
 GAAGTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCATCACAA
 CCGCTTTTCCACAATCATTTCTTCTTAAACAGGAATGATTATTGGTGGAGGACTGACA
 ATTCTTGGTTGTATTATTTTGGGAATTTTGTATTCTTTTAAAGAAAACATAAAATAGC
 AAATCTGAAAGAAACGATACAGTA

SEQ ID NO. 4502

STRAIN 090

GATACCCCTAATCAACTAACAATCACAC
 AGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTA
 TGGACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGA
 TAGCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATA
 CTAATGGTCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGT
 GCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGA
 ATTACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAA
 AAGTTGAAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAG
 ATAAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCAGAA
 TCAGCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGA
 TTACTTCATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTA
 TTACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTACCG
 TATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGG
 AAGTaGAGGTaGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAA
 CCATCACAAACCG

SEQ ID NO. 4503

STRAIN H36B

GATACCCCTAATCAACTAACAATCACACAGA
 TAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGG
 ACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATAG
 CGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACTA
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGTGCT
 TATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAATT
 ACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAAG
 TTGAAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGATA
 AAGAAAAGGCTwTCCGGAGTAATATTTGTATTATACGATAACCAGAATCA
 GCCAGTTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATTA
 CTTCAATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA
 CCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTAT
 ATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG
 TAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCA
 TCACAACCGC

SEQ ID NO. 4504

STRAIN 18RS21

GATACCCCTAATCAACTAACAATCACACAG
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
 GACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATA
 GCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
 AATGGTCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGTGCT
 TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT
 TACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAA
 GTTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGAT
 AAAGAAAAGGCTATCCGGAGTAATATTTGTATTATACGATAACCAGAATC
 AGCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATTT
 ACTTCATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATT
 ACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAA
 GTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACC
 ATCACAACC

SEQ ID NO. 4505

STRAIN CJB110

GATACCCCTAATCAACTAACAATCACACA
 GATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT
 GGACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGAT
 AGCGAATTGaACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATAC
 TAATGGTCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGTG
 CTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAA
 TTACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAA
 AGTTGAAACAGGCCGATTaaAACTTATTAAATATACAAAAGAAGGAAAGA

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

TAAAGAAAAGGCTaTCAGGAGTAATATTTGTATTATACGATAACCAGAAT
 CAGCCAGTTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGAT
 TACTTCATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTAT
 TACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTaCCGT
 ATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA
 AGTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAAC
 CATCACAACC

SEQ ID NO. 4506

STRAIN 1169NT

GATACCCCTAATCAACTAACAATCACACAG
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
 GACTGTGACTGACAACCTTAAAGTTGATTTATTGAGCCAAATGACAGATA
 GCGAATTGAACCAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
 AATGGtCagaCAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGC
 TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT
 TACCAGATGATAAGTTATCAAATCAATTACAGATAAAATCCTAAGCGAAAA
 GTTGAAAACAGGCCGATTAAAACTTATTAATATACAAAAGAAGGAAAGAT
 AAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCAGAATC
 AGCCAGTTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATT
 ACTTCATTAGTAAGTgaTGATAAGGGAGAAATTGAGGTTGAAGGTTTATT
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAA
 GTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACC
 ATCACAACC

PRETTY of: /biotmp/msa184750.2{*} May 13, 2003 06:23 ..

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      1                                     50
msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} atgaaaaaga ttagaaaaag tttaggactt ctactatggt gcttttttagg
msa184750.2{150_H36B} -----
      Consensus *****

      51                                     100
msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} attggtacaa ttagcggtttt tttcggttagc cagtgtaaat gctGATACCC
msa184750.2{150_H36B} -----
      Consensus *****

      101                                    150
msa184750.2{150_090} CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_1169NT} CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_CJB110} CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_18RS21} CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_2603} CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_H36B} CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
      Consensus *****

      151                                    200
msa184750.2{150_090} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_1169NT} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_CJB110} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_18RS21} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_2603} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_H36B} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
      Consensus *****

      201                                    250
msa184750.2{150_090} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_1169NT} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_CJB110} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_18RS21} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_2603} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_H36B} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
      Consensus *****

      251                                    300
msa184750.2{150_090} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_1169NT} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_CJB110} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_18RS21} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_2603} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_H36B} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
      Consensus *****

      301                                    350

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Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184750.2{150_090}	AATGGTTCGT	ACTTTGGTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_1169NT}	AATGGTTCGT	ACTTTGGTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_CJB110}	AATGGTTCGT	ACTTTGGTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_18RS21}	AATGGTTCGT	ACTTTGGTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_2603}	AATGGTTCGT	ACTTTGGTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_H36B}	AATGGTTCGT	ACTTTGGTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_1169NT}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_CJB110}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_18RS21}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_2603}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_H36B}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_1169NT}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_CJB110}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_18RS21}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_2603}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_H36B}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_1169NT}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_CJB110}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_18RS21}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_2603}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_H36B}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTwTCcG	GAGTAATATT
Consensus	*****	*****	*****	*****_**_*	*****
msa184750.2{150_090}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_1169NT}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_CJB110}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_18RS21}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_2603}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_H36B}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_1169NT}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_CJB110}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_18RS21}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_2603}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_H36B}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_1169NT}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_CJB110}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_18RS21}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_2603}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_H36B}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_1169NT}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_CJB110}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_18RS21}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_2603}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_H36B}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_1169NT}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_CJB110}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_18RS21}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_2603}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_H36B}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CCg-----	-----
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CC-----	-----

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

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msa184750.2{150_CJB110} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_18RS21} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_2603} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgCtttttc cacaatcatt
msa184750.2{150_H36B} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgC-----
Consensus *****

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801 850

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} tcttcctaaa acaggaatga ttattgggtgg aggactgaca attcttggtt
msa184750.2{150_H36B} -----
Consensus *****

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851 900

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} gtattatttt gggaattttg tttatctttt taagaaaaaac taaaaatagc
msa184750.2{150_H36B} -----
Consensus *****

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901 924

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} aaatctgaaa gaaacgatac agta
msa184750.2{150_H36B} -----
Consensus *****

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SEQ ID NO. 4507**STRAIN 2603**

MKKIRKSLGILLCCFLGLVQLAFFSVASVNADTPNQLTITQIGLQPNNTTEEGISYRLWTV
 TDNLKVDLLSQMTDSELNQKYKSILTSPTDTNGQTKIALPNGSYFGRAYKADQSVSTIVP
 FYIELPDDKLSNQLQINPKRKVETGRLKLIKYTEKGKIKKRLSGVIFVLYDNQNPVRFK
 NGRFTTDQDGITSLVTDKGEIEVEGLLPKGKIFREAKALTGYRISMKDAVVAVVANKTQ
 EVEVENEKETPPPTNPKPSQPLFPQSFLPKTGMII GGGLTILGCIILGILFIFLRKTKNS
 KSERNDTV

SEQ ID NO. 4508**STRAIN 090**

DTPNQLTITQIGLQPNNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTEKGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDQDGITSLVTDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQ

SEQ ID NO. 4509**STRAIN H36B**

DTPNQLTITQIGLQPNNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTEKGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDQDGITSLVTDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQ

SEQ ID NO. 4510**STRAIN 18RS21**

DTPNQLTITQIGLQPNNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTEKGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDQDGITSLVTDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQ

SEQ ID NO. 4511**STRAIN 1169NT**

DTPNQLTITQIGLQPNNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTEKGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDQDGITSLVTDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQ

PRETTY of: /biotmp/msa184868.2{*} May 13, 2003 06:25 ..

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msa184868.2{150_090} 1 ----- 50
msa184868.2{150_2603} mkkirkslgl llccflglvq laffsvasvn ~DTPNQLTIT QIGLQPNNTTE
msa184868.2{150_H36B} ----- ~DTPNQLTIT QIGLQPNNTTE
msa184868.2{150_1169NT} ----- ~DTPNQLTIT QIGLQPNNTTE
msa184868.2{150_18RS21} ----- ~DTPNQLTIT QIGLQPNNTTE
Consensus *****

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51 100

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msa184868.2{150_090} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP

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Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184868.2{150_2603}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_H36B}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_1169NT}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_18RS21}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
Consensus	*****	*****	*****	*****	*****
101					
msa184868.2{150_090}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRLKLI
msa184868.2{150_2603}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRLKLI
msa184868.2{150_H36B}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRLKLI
msa184868.2{150_1169NT}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRLKLI
msa184868.2{150_18RS21}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRLKLI
Consensus	*****	*****	*****	*****	*****
151					
msa184868.2{150_090}	KYTKEGKIKK	RLSGVIFVLY	DNQNPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_2603}	KYTKEGKIKK	RLSGVIFVLY	DNQNPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_H36B}	KYTKEGKIKK	RLSGVIFVLY	DNQNPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_1169NT}	KYTKEGKIKK	RLSGVIFVLY	DNQNPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_18RS21}	KYTKEGKIKK	RLSGVIFVLY	DNQNPVRFK	NGRFTTDQDG	ITSLVTDDKG
Consensus	*****	*****	*****	*****	*****
201					
msa184868.2{150_090}	EIEVEGLLP	KYIFREAKAL	TGYRISMKA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_2603}	EIEVEGLLP	KYIFREAKAL	TGYRISMKA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_H36B}	EIEVEGLLP	KYIFREAKAL	TGYRISMKA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_1169NT}	EIEVEGLLP	KYIFREAKAL	TGYRISMKA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_18RS21}	EIEVEGLLP	KYIFREAKAL	TGYRISMKA	VVAVVANKTQ	EVEVENEKET
Consensus	*****	*****	*****	*****	*****
251					
msa184868.2{150_090}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_2603}	PPPTNPKPSQ	plfpqsflpk	tgmiigggt	ilgciilgil	fiflrktkns
msa184868.2{150_H36B}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_1169NT}	PPPTNPKPSQ	-----	-----	-----	-----
msa184868.2{150_18RS21}	PPPTNPKPSQ	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
301					
msa184868.2{150_090}	-----	-----	-----	-----	-----
msa184868.2{150_2603}	kserndtv	-----	-----	-----	-----
msa184868.2{150_H36B}	-----	-----	-----	-----	-----
msa184868.2{150_1169NT}	-----	-----	-----	-----	-----
msa184868.2{150_18RS21}	-----	-----	-----	-----	-----
Consensus	*****	-----	-----	-----	-----

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

SEQ ID NO. 4601

STRAIN A909

TGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCAGGTGTAACCTATATTACCTTT
 CTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGAAATGCTTTTCGTCCAGA
 TAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTAAACGATATCATGA
 ATTTCTCGGAGATTTTATGCGTCAGTTCAGTCTAGGTGTAGCTGGGGCACATGGAAA
 AACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATTACAGACACTTCTTTCCT
 AATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTGTGTTTGAAGCTGA
 TGAATACGAACGTCAATTTTATGCCGTACCATCCAGAATACTCAATTATTACCAATATTGA
 TTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTCAATGCCTTTAATGACTA
 TGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAAGATCCAAAACCTCATGAAAT
 CACTTCTGAGGCACCAATATATTATTATGGTTTGAAGATTCAAATGATTTTATAGCAAA
 AGACATCACTCGAAGCTGTTAATGGTTCTGACTTTAAGGTTTTCTATAACCAAGAAGAAAT
 TGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATCTTAAATGCAACTGCTGTTAT
 TGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGCATTGGAAGACATT
 TTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACGATACTGTCAATTATTGATGA
 CTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTCGACAAAAATACCC
 GTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACTCGTACGATAGCTCTTTT
 AGACGAATTTGCCCATGCTTGGAGTCAAGCGGATAGCGTTTATCTCGCTCAAATATATGG
 TTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTTAGCTGCTAAGATTGT
 CAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTACTCAATCATGATAATGC
 TGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCTCTTTTGAAGAATT
 ATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4602

STRAIN 1169NT

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGC
 AGGTGTAACCTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGC
 AGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTA
 TCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCAGTCTAGG
 TGCTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAA
 TATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA
 TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCAATTTATGCCGTACCATCCAGAATA
 CTCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGT
 ATTTCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGA
 AGATCCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTGAAGA
 TTCAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGT
 TTTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATAT
 CTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCAATTAGT
 AGCTGAGCCTTTGAAGACATTTTCAAGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGA
 CGATACTGTCAATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA
 TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTT
 CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCCTTGAGTCAAGCGGATAGCGT
 TTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
 AGATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCC
 TTTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTA
 TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4603

STRAIN 090

AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCA
 GGTGTAACCTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
 GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
 CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCAGTCTAGGT
 GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAAT
 ATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
 TACTTTGTGTTTGAAGCTGATGAATACGAACGTCAATTTTATGCCGTACCATCCAGAATAC
 TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTA
 TTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAA
 GATTCAAAAACCTTCATGAAATCACTTCTAAGGCACCAATATATTATTATGGTTTGAAGAT
 TCAAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGT
 TTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATC
 TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCAATTAGTA
 GCTGAGCATTGGAAGACATTTTCAAGGGTAAACGTGTTTTACTGAGAAGATTATTGAC
 GATACTGTCAATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTT
 ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT
 TATCTTGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
 GATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
 TTAATCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4604

STRAIN H36B

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACTCAACGTGGTTTAGAGCAAGCAGGT
 ATAACCTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGA
 AATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAT
 TTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCAGTCTAGGTGTA
 GCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATT
 ACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTAC
 TTTGTGTTTGAAGCTGATGAATACGAACGTCAATTTTATGCCGTACCATCCAGAATACTCA
 ATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTC
 AATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAAGAT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

CCAAAAC^{TTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATTCA}
 AATGATTTTATAGCAAAAGATATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTTC
 TATAACCAAGAAGAAATTGGTTCAGTTTCACGTACCAGCATACGGTAAACATAATATCTTA
 AATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCT
 GAGCATTGGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAAATTATTGACGAT
 ACTGTCAATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCT
 GCTCGACAAAAATACCCGTCAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACT
 CGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTAT
 CTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGAT
 TTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTA
 CTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATGAG
 CGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4605

STRAIN 18RS21

AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCA
 GGTGTAACATATATTACCTTTCTACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
 GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
 CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
 GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAAT
 ATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
 TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
 TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTA
 TTCAATGCCCTTAAATGACTATGCTAAGCAAGTTCAAAGGTTTATTCAATTTATGGAGAA
 GATCCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGAT
 TCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
 TTCTATAACCAAGAAGAAATTGGTCAGTTTTCATGTACCAGCATACGGTAAACATAATATC
 TTAAATGCAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
 GCTGAGCATTGGAAGACGTTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGAC
 GATACTGTCAATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
 GCTGCTCGACAAAAATACCCGTCAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTT
 ACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTT
 TATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
 GATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
 TTAATCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTAT
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4606

STRAIN M732

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCAG
 GTGTAACATATATTACCTTTCTACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
 GAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
 ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTG
 TAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATA
 TTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATT
 ACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACT
 CAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTAT
 TCAATGCCCTTAAATGACTATGCTAAGCAAGTTCAAAGGTTTATTCAATTTATGGAGAAG
 ATCCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATT
 CAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTT
 TCTATAACCAAGAAGAAATTGGTCAGTTTTCATGTACCAGCATACGGTAAACATAATATCT
 TAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAG
 CTGAGCATTGGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACG
 ATACTGTCAATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATG
 CTGCTCGACAAAAATACCCGTCAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCA
 CTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTT
 ATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAG
 ATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTT
 TACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATG
 AGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4607

STRAIN M781

AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCAG
 GTGTAACATATATTACCTTTCTACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
 GAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
 ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
 GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAA
 TATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA
 TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
 CTCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGT
 ATTCAATGCCCTTAAATGACTATGCTAAGCAAGTTCAAAGGTTTATTCAATTTATGGAGA
 AGATCCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGA
 TTCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT
 TTTCTATAACCAAGAAGAAATTGGTCAGTTTTCATGTACCAGCATACGGTAAACATAATAT
 CTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT
 AGCTGAGCATTGGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGA
 CGATACTGTCAATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA
 TGCTGCTCGACAAAAATACCCGTCAAAGAAATTGTAGCTATTTTCCAACCGCATACGTT
 CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGT
 TTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
 AGATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCC
 TTTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4608

STRAIN CJB110

AAAAAGCAGGCTCTAGTGACGTTGACAAATATATATTTTACCCAACGTGGTTTAGAGCAAGCA
GGTGTAACTATATTACCTTTCTCACC GAATAATATCAGTGAGGATTTAGAGATTATTGCA
GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
ATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTA
TTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAA
GATTCAAAACTTCATGAAATCACTTCTAAGGCACCAATATATTATTATGGTTTGAAGAT
TCAATGATTTTATAGCAAAAGACATCACTCGAAGTGTAAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTTGGTCAGTTTTCATGTACCAGCATACGGTAAACATAATATC
TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGCATTTGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAGATTATTGAC
GATACTGTCAATTTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
GCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGTACTATTTTCCAACCGCATACGTTT
ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT
TATCTTGCTCAATATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
GATTTAGCTGCTAAGATTGTCAAACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4609

STRAIN JM9130013 (reverse complement)

GTTCAAAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACTCAACGTGGTTTAGA
GCAAGCAGGTATAACTATATACCTTTCTCACC GAATAATATCAGTGAGGATTTAGAGAT
TATTGTCAGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAA
GGGCTATCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAG
TCTAGGTGTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTT
AAAAAATATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAA
TGCTAATTACTTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCC
AGAATACTCAATTATTATACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGA
GGACGTATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTA
TGGAGAAGATCCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATATTATGGTTT
TGAAGATTCAATGATTTTATAGCAAAAGATATCACTCGAAGTGTAAATGGTTCTGACTT
TAAGGTTTTCTATAACCAAGAAGAAATTTGGTCAGTTTTCAGTACCAGCATACGGTAAACA
TAATATCTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGC
ATTAGTAGCTGAGCATTTGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAAAT
TATTGACGATACTGTCAATTTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGAC
ATTAGATGCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGTACTATTTTCCAACCGCA
TACGTTCACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGA
TAGCGTTTATCTCGCTCAATATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAA
GGTAGAAGATTTAGCTGCTAAGATTGTCAAACTCAGATTTAGTGACAGTCGAAAATGT
CTCGCCTTTACTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCA
ATTGTATGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4610

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATATTTTACCCAACGTGGTTTAGAGCAAGCAGGTGTAA
CTATATTACCTTTCTCACC GAATAATATCAGTGAGGATTTAGAGATTATTGTCAGGAAATG
CTTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTA
AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG
GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAG
ACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTTACTTTG
TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA
TTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTCAATG
CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAAGATCCAA
AACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTGAAGATTCAAATG
ATTTTATAGCAAAAGACATCACTCGAAGTGTAAATGGTTCTGACTTTAAGGTTTCTATA
ACCAAGAAGAAATTTGGTCAGTTTTCATGTACCAGCATACGGTAAACATAATATCTTAAATG
CAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC
ATTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACGATACTG
TCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC
GACAAAAATACCCGTCAAAAGAAATTTAGTACTATTTTCCAACCGCATACGTTCACTCGTA
CGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGATAGCGTTTATCTCG
CTCAATATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTAG
CTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTACTCA
ATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT
CTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4611

STRAIN 2603

atgtcaaaaacttatcattttattggtattaaaggatccggaatgagtgccttagcactg
atgcttcatcaaatgggacataacgtccaaggaagtgcgttgacaaatattattttacc
caacgtgggttagagcaagcaggtgtaactatattacctttctcaccgaataatcagtc
gaggatttagagattattgcaggaatgcttttcgtccagataacaatgaagagttggct
tatgttattgaaaagggtatcaatttaaacgatcatgaattttctcgagattttatg
cgtcagttcactagtcaggtgtagctggggcacatggaaaaacctcaacgacaggttta
ttagctcatgttttaaaaaatattacagacacttctttcctaattggagatggtacagga

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

cgtgggtctgctaattgctaattactttgtggttgaagctgatgaatacgaacgctcatttt
 atgccgtaccatccagaataactcaattattaccaatattgattttgaccatcctgattat
 ttacaggttagaggacgtattcaatgccttttaagtactatgctaagcaagttcaaaaa
 gggtttattcattttatggagaagatccaaaacttcatgaaatcacttctgaggcaccaata
 tattattatgggtttgaagattcaaatgattttatagcaaaagacatcactcgaactgtt
 aatgggtctgactttaaggtttctataaccaagaagaattgggtcagtttcatgtacca
 gcatacggtaaacataatatcttaaatgcaactgctgttattgctaacctttacataatg
 ggaattgatatggcatttagtagctgagcatttgaagacgtttcaggggtaaaagcgtcgt
 ttactgagaagattattgacgatactgtcattattgatgactttgctcaccatcctact
 gagattattgacgacatttagatgctgctcgacaaaaataccgctcaaaagaattgtagct
 attttccaaccgcatacgttcaactcgtacgatagctcttttagacgaatttgcccatgcc
 ttgagtcgaagcggatagcgtttatctcgctcaaatatatgggtctgctagagaagtagat
 aatgggtgaggtgaaggtagaagatttagctgctaagattgtcaaacactcagatttagtg
 acagtcgaaaatgtctcgctttactcaatcatgataatgctgtctatgtctttatgggt
 gctggagacattcaattgtatgagcgtcttttgaagaattattagctaacctaaactaaa
 aatacacia

SEQ ID NO. 4612

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATATTTTACCCAACGTGGTCTTAGAGCAAGCAGGTGTAA
 CTATATTACCTTTCTCACC GAATAATATCAGTGAGGATTTAGAGATTATTGCAGGAAATG
 CTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTA
 AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG
 GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAATATTACAG
 AACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTCTGCTAATGCTAATTACTTTG
 TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA
 TTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTCAATG
 CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAITTTATGGAGAAGATCCAA
 AACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATTCAAATG
 ATTTTATAGCAAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTCTATA
 ACCAAGAAGAAATTGGTCAGTTTCATGTACAGCAGCATACGGTAAACATAATATCTTAAATG
 CAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC
 ATTTGAAGACATTTTCAAGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACGATACTG
 TCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC
 GACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACTCGTA
 CGATAGCTCTTTTAGACGAATTTGCCATGCCCTTGAGTCAAGCGGATAGCGTTTATCTCG
 CTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTAG
 CTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCAAAAATGTCTCGCCTTTACTCA
 ATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT
 CTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

PRETTY of: /biotmp/msa56524.2(*) November 26, 2002 08:06 ..
 PRETTY of: /biotmp/msa253045.2(*) January 31, 2003 03:51 ..

	1		50
msa253045.2{157_090}	-----	-----	-----
msa253045.2{157_CJB110}	-----	-----	-----
msa253045.2{157_H36B}	-----	-----	-----
msa253045.2{157_JM9130013}	-----	-----	-----
msa253045.2{157_1169NT}	-----	-----	-----
msa253045.2{157_A909}	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----
msa253045.2{157_M732}	-----	-----	-----
msa253045.2{157_M781}	-----	-----	-----
msa253045.2{157_18RS21}	-----	-----	-----
msa253045.2{157_2603}	atgtcaaaaa	cttatcattt	tattgggtatt
Consensus	*****	*****	*****
	51		100
msa253045.2{157_090}	-----	-----	-aaagcaggc
msa253045.2{157_CJB110}	-----	-----	Aaaagcaggc
msa253045.2{157_H36B}	-----	-----	Aaaagcaggc
msa253045.2{157_JM9130013}	-----	-----	GttcaA
msa253045.2{157_1169NT}	-----	-----	Aaaagcaggc
msa253045.2{157_A909}	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----caggc
msa253045.2{157_M732}	-----	-----	Aaaagcaggc
msa253045.2{157_M781}	-----	-----	-aaagcaggc
msa253045.2{157_18RS21}	-----	-----	-aaagcaggc
msa253045.2{157_2603}	cctagcactg	atgcttcac	aaatGggacA
Consensus	*****	*****	*****
	101		150
msa253045.2{157_090}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_CJB110}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_H36B}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_JM9130013}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_1169NT}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_A909}	-TGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_COH1}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_M732}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_M781}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_18RS21}	tTGACAAATA	TTATTTTACc	CAACGTGGTT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_2603}	tTGACAAATA	TTATTTTACC	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_CJB110}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_H36B}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_JM9130013}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_1169NT}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_A909}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_COH1}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M732}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M781}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_18RS21}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_2603}	ATATTACCTT	TCTCACCAGAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_CJB110}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_H36B}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_JM9130013}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_1169NT}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_A909}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_COH1}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M732}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M781}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_18RS21}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_2603}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_CJB110}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_H36B}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_JM9130013}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_1169NT}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_A909}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_COH1}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M732}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M781}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_18RS21}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_2603}	AAAAGGGCTA	TCAATTTAAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_CJB110}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_H36B}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_JM9130013}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_1169NT}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_A909}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_COH1}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M732}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M781}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_18RS21}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_2603}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_CJB110}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_H36B}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_JM9130013}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_1169NT}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_A909}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_COH1}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_M732}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_M781}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_18RS21}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
msa253045.2{157_2603}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCTTTCC
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_CJB110}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_H36B}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_JM9130013}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_1169NT}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_A909}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_COH1}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M732}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M781}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_18RS21}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_2603}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_CJB110}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_H36B}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_JM9130013}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_1169NT}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_A909}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_COH1}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M732}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M781}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_18RS21}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_2603}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_CJB110}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_H36B}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_JM9130013}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_1169NT}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_A909}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_COH1}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M732}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M781}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_18RS21}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_2603}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_CJB110}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_H36B}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_JM9130013}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_1169NT}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_A909}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_COH1}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M732}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M781}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_18RS21}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_2603}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	GGTTTATTCA	TTTATGGAGA	AGATtCAAAA	CTTCATGAAA	TCACCTTCTaA
msa253045.2{157_CJB110}	GGTTTATTCA	TTTATGGAGA	AGATtCAAAA	CTTCATGAAA	TCACCTTCTaA
msa253045.2{157_H36B}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_JM9130013}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_1169NT}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_A909}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_COH1}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_M732}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_M781}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_18RS21}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
msa253045.2{157_2603}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTTCTgA
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_CJB110}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_H36B}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_JM9130013}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_1169NT}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_A909}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_COH1}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M732}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M781}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_18RS21}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_2603}	GGCACCATA	TATTATTATG	GTTTTGAAGA	TTCAAATGAT	TTTATAGCAA
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_CJB110}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_H36B}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_JM9130013}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_1169NT}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_A909}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_COH1}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_M732}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M781}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_18RS21}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_2603}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
Consensus	****-*****	*****	*****	*****	*****
msa253045.2{157_090}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_CJB110}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_H36B}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_JM9130013}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_1169NT}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_A909}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_COH1}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_M732}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_M781}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_18RS21}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_2603}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
Consensus	*****	*****	***-*****	*****	*****
msa253045.2{157_090}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_CJB110}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_H36B}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_JM9130013}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_1169NT}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_A909}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_COH1}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_M732}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_M781}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_18RS21}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
msa253045.2{157_2603}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_CJB110}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_H36B}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_JM9130013}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_1169NT}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_A909}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_COH1}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_M732}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_M781}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_18RS21}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_2603}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCGT
Consensus	*****	*****	*****-*	*****	***-*****
msa253045.2{157_090}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_CJB110}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_H36B}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_JM9130013}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_1169NT}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_A909}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_COH1}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_M732}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_M781}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_18RS21}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_2603}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
Consensus	*****	*-*****	*****	*****	*****
msa253045.2{157_090}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_CJB110}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_H36B}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_JM9130013}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_1169NT}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_A909}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_COH1}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_M732}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_M781}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_18RS21}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_2603}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_CJB110}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_H36B}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_JM9130013}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_1169NT}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_A909}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_COH1}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M732}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_M781}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_18RS21}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
msa253045.2{157_2603}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACTCGTACG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1051 ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	1100 CGGATAGCGT
msa253045.2{157_CJB110}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_H36B}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_JM9130013}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_1169NT}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_A909}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_COH1}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_M732}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_M781}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_18RS21}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_2603}	ATAGCTCTTT	TAGACGAATT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1101 TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	1150 AATGGTGAGG
msa253045.2{157_CJB110}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_H36B}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_JM9130013}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_1169NT}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_A909}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_COH1}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_M732}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_M781}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_18RS21}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_2603}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1151 TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	1200 AGATTTAGTG
msa253045.2{157_CJB110}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_H36B}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_JM9130013}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_1169NT}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_A909}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_COH1}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_M732}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_M781}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_18RS21}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_2603}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1201 ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	1250 CTGTCTATGT
msa253045.2{157_CJB110}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_H36B}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_JM9130013}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_1169NT}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_A909}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_COH1}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_M732}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_M781}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_18RS21}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_2603}	ACAGTCGAAA	ATGTCTCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1251 CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	1300 TTTGAAGAAT
msa253045.2{157_CJB110}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_H36B}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_JM9130013}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_1169NT}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_A909}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_COH1}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_M732}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_M781}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_18RS21}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_2603}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1301 TATTAGCTAA	CCTAACTAAA	AATACACAA	1329	
msa253045.2{157_CJB110}	TATTAGCTAA	CCTAACTAAA	AATACACAA		
msa253045.2{157_H36B}	TATTAGCTAA	CCTAACTAAA	AATACACAA		
msa253045.2{157_JM9130013}	TATTAGCTAA	CCTAACTAAA	AATACACAA		
msa253045.2{157_1169NT}	TATTAGCTAA	CCTAACTAAA	AATACACAA		
msa253045.2{157_A909}	TATTAGCTAA	CCTAACTAAA	AATACACAA		

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_COH1}	TATTAGCTAA CCTAACTAAA AATACACAA
msa253045.2{157_M732}	TATTAGCTAA CCTAACTAAA AATACACAA
msa253045.2{157_M781}	TATTAGCTAA CCTAACTAAA AATACACAA
msa253045.2{157_18RS21}	TATTAGCTAA CCTAACTAAA AATACACAA
msa253045.2{157_2603}	TATTAGCTAA CCTAACTAAA AATACACAA
Consensus	*****

SEQ ID NO. 4613**STRAIN A909 frame: 2**

DKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHFKRYHE
 FLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANANYFVFEAD
 EYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEI
 TSEAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKHNILNATAVI
 ANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLDAARQKYP
 SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIV
 KHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4614**STRAIN 1169NT frame: 2**

KAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYP SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4615**STRAIN 090 FRAME:1**

KAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DSKLHEITSKAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYP SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4616**STRAIN H36B frame: 2**

KAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYP SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4617**STRAIN 18RS21 frame: 1**

KAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYP SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4618**STRAIN M732 frame: 2**

KAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYP SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4619**STRAIN JM9130013 frame: 2**

FKKAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEK
 GYHFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSAN
 ANYFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIY
 GEDPKLHEITSEAPIYYYGFEDSNDFAKDI TRTVNGSDFKVFYNQEEIGQFHVPAVGKH
 NILNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIAT
 LDAARQKYP SKEIVAI FQPHFTFTRTIALLLDEFAHALSQADSVYLAQIYGSAREVDNGEVK
 VEDLAAKIVKHSDDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4620**STRAIN M781 frame: 1**

KAGSSDVKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAVGKHNI
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYPskeivAI FQPHFTFRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSIDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4621

STRAIN CJB110 frame: 3

KAGSSDVdkyyftQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DSKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAVGKHNI
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
 AARQKYPskeivAI FQPHFTFRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSIDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4622

STRAIN 2603 frame: 1

MSKTYHFIGIKGSGMSALALMLHQMGNVQGSVDKYYFTQRGLEQAGVTILPFSPNNIS
 EDLEIIAGNAFRPDNNEELAYVIEKGYQFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGL
 LAHVLKNITDTSFLIGDGTGRGSANANYFVFEADEYERHFMPYHPEYSIIITNIDFDHPDY
 FTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEITSEAPIYYYGFEDSNDFIAKDITRTV
 NGSDFKVFYNQEEIGQFHVPAVGKHNI LNATAVIANLYIMGIDMALVAEHLKTFSGVKRR
 FTEKIIDDTVIIDDFAHHPTEIIATLDAAARQKYPskeivAI FQPHFTFRTIALLDFAHA
 LSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIVKHSIDLVTVENVSPLLNDNAVYVFMG
 AGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4623

STRAIN COH1 frame: 3

GSSDVdkyyftQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHF
 KRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANANYF
 VFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDP
 KLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAVGKHNI LN
 ATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLDAA
 RQKYPskeivAI FQPHFTFRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVEDL
 AAKIVKHSIDLVTVENVSPLLNDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

PRETTY of: /biotmp/msa56635.2{*} November 26, 2002 08:08 ..

	1				50
msa253220.2{157_090}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_CJB110}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_1169NT}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_18RS21}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_M732}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_M781}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_COH1}	-----	-----	-----	-----g	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_H36B}	-----	-----	-----	-----kag	ssdvDKYYFT QRGLEQAGiT
msa253220.2{157_JM9130013}	-----	-----	-----	-----fkag	ssdvDKYYFT QRGLEQAGiT
msa253220.2{157_2603}	msktyhfigi	kgsgmsalal	mlhqmghnvq	gsdvDKYYFT	QRGLEQAGvT
msa253220.2{157_A909}	-----	-----	-----	-----DKYYFT	QRGLEQAGvT
Consensus	*****	*****	*****	-----	*****
	51				100
msa253220.2{157_090}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_CJB110}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_1169NT}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_18RS21}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_M732}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_M781}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_COH1}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_H36B}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_JM9130013}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
msa253220.2{157_2603}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYqFK	RYHEFLGDFM
msa253220.2{157_A909}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA	YVIEKGYhFK	RYHEFLGDFM
Consensus	*****	*****	*****	*****	*****
	101				150
msa253220.2{157_090}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_CJB110}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_1169NT}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_18RS21}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_M732}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_M781}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_COH1}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_H36B}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_JM9130013}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_2603}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
msa253220.2{157_A909}	RQFTSLGVAG	AHGKTSTTGL	LAHVLKNITD	TSFLIGDGTG	RGSANANYFV
Consensus	*****	*****	*****	*****	*****
	151				200
msa253220.2{157_090}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253220.2{157_CJB110}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_1169NT}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_18RS21}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M732}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M781}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_COH1}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_H36B}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_JM9130013}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_2603}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_A909}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
Consensus	*****	*****	*****	*****	*****
201					
msa253220.2{157_090}	GLFIYGEDsK	LHEITSkAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_CJB110}	GLFIYGEDsK	LHEITSkAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_1169NT}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_18RS21}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_M732}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_M781}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_COH1}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_H36B}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_JM9130013}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_2603}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_A909}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
Consensus	*****	*****	*****	*****	*****
251					
msa253220.2{157_090}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_CJB110}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_1169NT}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_18RS21}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M732}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M781}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_COH1}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_H36B}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_JM9130013}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_2603}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_A909}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
Consensus	*****	*****	*****	*****	*****
301					
msa253220.2{157_090}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_CJB110}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_1169NT}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_18RS21}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_M732}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_M781}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_COH1}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_H36B}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_JM9130013}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_2603}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
msa253220.2{157_A909}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeiva	IFQPHTFTRT
Consensus	*****	*****	*****	*****	*****
351					
msa253220.2{157_090}	IALLDgFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_CJB110}	IALLDgFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_1169NT}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_18RS21}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_M732}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_M781}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_COH1}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_H36B}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_JM9130013}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_2603}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_A909}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
Consensus	*****	*****	*****	*****	*****
401					
msa253220.2{157_090}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_CJB110}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_1169NT}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_18RS21}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M732}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M781}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_COH1}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_H36B}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_JM9130013}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_2603}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_A909}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
Consensus	*****	*****	*****	*****	***

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)**SEQ ID NO. 4701****STRAIN A909**

TATTTTTTAACAACAAAAAAGGAAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4702**STRAIN H36B**

TATTTTTTTAACAACAAAAAAGGAAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4703**STRAIN 18RS21**

TATTTTTTTAACAACAAAAAAGGAAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4704**STRAIN M732**

TATTTTTTTAACAACAAAAAAGGAAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4705**STRAIN COH1**

TATTTTTTTAACAACAAAAAAGGAAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4706**STRAIN M781**

TATTTTTTTAACAACAAAAAAGGAAAAAGAGC
 TAAGGAAAAATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAA
 GAATATCATCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGC
 TGTGATACTTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGA
 CAACAGAGGATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTT
 GACTTTGCTAATGATTTTGTCATCAAGCTAAATCAAAATTTCTCAGACGA
 GGATACTGCTAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATA
 TTGTCATTGATTATAAAGAAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4707**STRAIN 2603**

tatttttttaacaacaaaaaaaggaaaagagctaaggaaaaatgcagaaaa
 attctatggagaatataaagaaaaatccagaagaatcatcaaataagcta
 aagataaagcaagtgaatattcaaatttagctgttgatacttttaaagat
 tataaagggtaaatttgaatcaggtgaattgacaacagaggatatcgctctc
 agccgttaaggaaaaaagcggagaagtagttgactttgctaattgattttg
 tcaatcaagctaaatcaaaattctcagacgaggatactgctaaaaaagaa
 gataaggctcctgaaacaaaagtagaagatatgtcattgattataaaga
 aaacacagaagataaagaaaaa

SEQ ID NO. 4708**STRAIN 090**

TATTTTTTTaACaACAAAAAAGGAAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGCTAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4709

STRAIN CJB110

TATTTTAAACAAACAAAAAAGGAAAAGAGCTAAGGAAAA
 ATGCAGAAAAATTTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCAT
 CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATAC
 TTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGG
 ATATCGTCTCAGCCGTAAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCT
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC
 TAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTG
 ATTATAAAGAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4710

STRAIN 1169NT

TATTTTAAACAAACAAAAAAGGAAAAGAGCTAAGGAAAA
 AATGCAGAAAAATTTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCA
 TCAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATA
 CTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAG
 GATATCGTCTCAGCCGTAAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCT
 TAATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC
 CTAAAAAAGAAAAAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATT
 GATTATAAAGAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4711

STRAIN JM9130013

TATTTTAAaCAACAAAAAAGGAAAAGAGCTAAGGAAAA
 ATGCAGAAAAATTTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCAT
 CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATAC
 TTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGG
 ATATCGTCTCAGCCGTAAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCT
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC
 TAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTG
 ATTATAAAGAAAACACAGAAGATAAAGAAAAA

PRETTY of: /biotmp/msa68511.2{*} January 22, 2003 05:47 ..

	1		50
msa68511.2{164_090}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_18RS21}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_2603}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_A909}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_CJB110}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_COH1}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_H36B}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_JM9130013}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_M732}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_M781}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
msa68511.2{164_1169NT}	TATTTTAA	CAACAAAAAA AGGAAAAGAG CTAAGGAAAA	ATGCAGAAAA
Consensus	*****	*****	*****
	51		100
msa68511.2{164_090}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_18RS21}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_2603}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_A909}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_CJB110}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_COH1}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_H36B}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_JM9130013}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_M732}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_M781}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
msa68511.2{164_1169NT}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT	CAAATAGCTA
Consensus	*****	*****	*****
	101		150
msa68511.2{164_090}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_18RS21}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_2603}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_A909}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_CJB110}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_COH1}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_H36B}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_JM9130013}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_M732}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_M781}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
msa68511.2{164_1169NT}	AAGATAAAGC	AAGTGAATAT TCAAATTTAG CTGTTGATAC	TTTTAAAGAT
Consensus	*****	*****	*****

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

	151		200
msa68511.2{164_090}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_18RS21}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_2603}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_A909}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_CJB110}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_COH1}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_H36B}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_JM9130013}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_M732}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_M781}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
msa68511.2{164_1169NT}	TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC		
Consensus	*****	*****	*****
	201		250
msa68511.2{164_090}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_18RS21}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_2603}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_A909}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_CJB110}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_COH1}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_H36B}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_JM9130013}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_M732}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_M781}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
msa68511.2{164_1169NT}	AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG		
Consensus	*****	*****	*****
	251		300
msa68511.2{164_090}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_18RS21}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_2603}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_A909}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_CJB110}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_COH1}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_H36B}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_JM9130013}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_M732}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_M781}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
msa68511.2{164_1169NT}	TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA		
Consensus	*****	*****	*****
	301		350
msa68511.2{164_090}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_18RS21}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_2603}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_A909}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_CJB110}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_COH1}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_H36B}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_JM9130013}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_M732}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_M781}	gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
msa68511.2{164_1169NT}	aATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA		
Consensus	-*****	*****	*****
	351		372
msa68511.2{164_090}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_18RS21}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_2603}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_A909}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_CJB110}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_COH1}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_H36B}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_JM9130013}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_M732}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_M781}	AAACACAGAA GATAAAGAAA AA		
msa68511.2{164_1169NT}	AAACACAGAA GATAAAGAAA AA		
Consensus	*****	*****	**

SEQ ID NO. 4712

STRAIN 2603

YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4713

STRAIN A909 frame: 1

YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4714

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

STRAIN H36B frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4715
 STRAIN 18RS21 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4716
 STRAIN M732 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4717
 STRAIN COH1 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4718
 STRAIN M781 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4719
 STRAIN 090 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4720
 STRAIN CJB110 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4721
 STRAIN 1169NT frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

SEQ ID NO. 4722
 STRAIN JM9130013 frame: 1
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFA~~NDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE~~
 DKEK

PRETTY of: /biotmp/msa68746.2{*} January 22, 2003 05:54 ..

	1		50
msa68746.2{164_090}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_1169NT}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_18RS21}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_2603}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_A909}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_CJB110}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_COH1}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_H36B}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_JM9130013}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_M732}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
msa68746.2{164_M781}	YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD		
Consensus	*****		
	51		100
msa68746.2{164_090}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_1169NT}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_18RS21}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_2603}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_A909}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_CJB110}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_COH1}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_H36B}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_JM9130013}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_M732}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		
msa68746.2{164_M781}	YKGGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE		

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

Consensus	*****	*****	*****	*****	*****
	101			124	
msa68746.2{164_090}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_1169NT}	nKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_18RS21}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_2603}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_A909}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_CJB110}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_COH1}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_H36B}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_JM9130013}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_M732}	dKAPETKVED	I	VIDYKENTE	DKEK	
msa68746.2{164_M781}	dKAPETKVED	I	VIDYKENTE	DKEK	
Consensus	-*****	*****	****		

Table 48: Comparative Sequences relating to SAG1474

SEQ ID NO: 4801

STRAIN 2603

aatagtactgagacaagtgccttcagtagttcctactacaaatactatcgt
tcaaactaatgacagtaatcctaccgcaaaatttgatcagaatcaggac
aatctgtaataggtcaagtaaaaccagataattctgcggcgcttacaaca
gttgacacgcctcatcatatttcagctccagatgcttataaaacaactca
atcaagtcctgtcgttgagagtaacttctactaagttaactgaagagactt
acaaacaaaaagatgggtcaagatttagccaacatgggtgagaagtggtcaa
gttactagttaggaactcgttaatatggcatatcgatattatttgctaaaga
aaacccatctttaaatagcagtcattactactagacgccaagaagctattg
aagaggctagaaaaacttaagataccaatcagccgcttttaggtgttccc
ttgttagtcaaggggttagggcacagatttaaagggtggtgaaaccaataa
tggttgatctatgcagatggaaaaattagcacatttgacagtagctatg
tcaaaaaatataaagatttaggatttattattttaggacaaacgaacttt
ccagagtatgggtggcgtaataaacagatttctaatttatacgggtctaac
gcataatccttgggatcttgcctcataatgctgggtggctcttctgggtggaa
gtgcagcagccattgctagcgggaatgacgccaattgctagcggtagtgat
gctgggtggttctatccgtattccatctcttggacgggcttggtaggttt
aaaaccaacaagaggattgggtgagtaaatgaaaagccagattcgtatagta
cagcagttcattttccattactaagtcattctagagacgcagaaacatta
ttaacttatctaagaaaagcgatcaaacgctagtatcagttaatgattt
aaaatctttaccaattgcttatactttgaaatcaccaatgggaacagaag
ttagtcaagatgctaaaaacgctattatggacaacgtcacattcttaaga
aaacaaggattcaaagtaacagagatagacttaccaattgatggtagagc
attaatgcgtgattattcaaccttggctattggcatgggaggagcttttt
caacaattgaaaaagacttaaaaaaacatgggtttactaaagaagacgtt
gatcctattacttgggcagttcatgttatttatcaaaattcagataaaggc
tgaacttaagaaatctattatggaagcccaaaacatattggatgattatc
gtaaggcaatggagaagcttcacaagcaatttctctatttcttatcgcca
acgaccgcaagtttagccctctaaatacagatccatattgtaacagagga
agataaaagagcgatttataatattggaacttgagccaagaagaaagaa
ttgctctctttaaatacgccagtgaggagcctatgttgcgtagaacaccttt
acacaaattgctaatatgacaggactccagctatcagtatcccgactta
cttatctgagtcgtggtttacccatagggacgatgttaatggcaggtgcaa
actatgatattggtatttaattaaatttgcaacttctttgaaaaacatcat
ggtttttaattggttaaatggcaagaataatagataaagaagtgaaccatc
tactggcctaatacagcctaactaactccctctttaaagctcattcatcat
tagtaaaatttagaagaaaattcacaagttactcaagtatctatctctaaa
aaatggatgaaatcgtctgttaaaaataaaccatccgtaatggcatatca
aaaagca

SEQ ID NO: 4802

STRAIN 090

AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAA
ATACTATCGTTCAAACATAATGACAGTAATCCTACCGCAAAATTTGTATCA
GAATCAGGACAATCTGTAATAGGTCAAGTAAAACCAGATAATTCTGCGGC
GCTTACAACAGTTGACACGCCTCATCATATTTAGCTCCAGATGCTTTAA
AAACAACCTCAATCAAGTCCTGTGCTTGAGAGTACTTCTACTAAGTTAACT
GAAGAGACTTACAAACAAAAGATGGTAAAGATTTAGCCAACATGGTGAG
AAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATAACGATATTA
TTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAA
GAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATACCAATCAGCCGTTTTT
AGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTG
AAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGAC
AGTAGCTATGTCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACA
AACGAACCTTTCCAGAGTATGGGTGGCGTAATATAACAGATTCTAAATTAT
ACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCT
TCTGGTGAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAG
CGGTAGTGATGCTGGTGGTTCTATCCGTATTCCATCTTCTTGGACGGGCT
TGGTAGGTTTAAAAACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGAT
TCGTATAGTACAGCAGTTTATTTCCATTAACTAAGTCATCTAGAGACGC
AGAAACATTATTAACTTATCTAAAGAAAAGCGATCAAACGCTAGTATCAG
TTAATGATTTAAAATCTTACCAATTGCTTATACTTTGAAATCACCAATG
GGAACAGAAGTTAGTCAAGATGCTAAAAACGCTATTATGGACAACGTCAC
ATTCTTAAGAAAAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTG
ATGGTAGAGCATTAAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGA
GGAGCTTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTTACTAA
AGAAGACGTTGATCCTATTACTTGGGCAGTTTATGTTATTTATCAAAATT
CAGATAAGGCTGAACTTAAGAAATCTATTATGGAAGCCCCAAAACATATG
GATGATTATCGTAAGGCAATGGAGAAGCTTCAAGCAATTTCTTATTTT
CTTATCGCCAACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATG
TAACAGAGGAAGATAAAGAGCGATTTATAATATGGAACCTTGGCCAA
GAAGAAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAG
AACACCTTTTACACAAATTGCTAATATGACAGGACTCCAGCTATCAGTA
TCCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATG
CGAGGTGCAAACTATGATATGGTATTAAATTAAATTTGCAACTTTCTTTGA
AAAACATCATGGTTTTAATGTTAAATGGCAAGAATAATAGATAAAGAAG
TGAAACCATCTACTGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCT
CATTTCATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATC
TATCTCTAAAAAATGGATGAAATCGTCTGTAAAAATAAACCATCCGTAA
TGGCATATCAAAAAGCA

SEQ ID NO: 4803

Table 48: Comparative Sequences relating to SAG1474

STRAIN A909

TACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAAT
 TTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAAACAGATAAT
 TCTGCGGCGCTTACAACAGTTGACACGCTCATCATATTTAGCTCCAGA
 TGCTTTAAAAACAACCTCAATCAAGTCCTGTGCTTGAGAGTACTTCTACTA
 AGTTAACTGAAGAGACTTACAAACAAAAAGATGGTCAAGATTTAGCCAAC
 ATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATA
 CGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTA
 GACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAG
 CCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCACAGTATTAA
 AGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCA
 CATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGATTTATTATT
 TTAGGACAAACGAACCTTTCCAGAGTATGGGTGGCGTAATATAACAGATTC
 TAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTG
 GTGGCTCTTCTGGTGGAAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCA
 ATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCCATCTTCTTG
 GACGGGCTTGGTAGGTTTAAAAACCAACAAGAGGATGGTGAGTAATGAAA
 AGCCAGATTCTGTATAGTACAGCAGTTTCATTTTCCATTAACTAAGTCATCT
 AGAGACGCAGAAACATTATTAACTTATCTAAAGAAAAGCGATCAAACGCT
 AGTATCAGTTAATGATTAAAAATCTTTACCAATTGCTTATACTTTGAAAT
 CACCAATGGGAACAGAACTTAGTCAAGATGCTAAAAACGCTATTATGGAC
 AACGTCACATTCTTAAGAAAACAAGGATTCAAAGTAACAGAGATAGACTT
 ACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCTTGGCTATTG
 GCATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAAAACATGGT
 TTTACTAAAGAAGACGTTGATCCTATTACTTGGGCAGTTTCATGTTATTTA
 TCAAAATTTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAA
 AACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTT
 CCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCCTCTAAATACAGA
 TCCATATGTACAGAGGAAGATAAAAGAGCGATTTATAATATGGAAAACT
 TGAGCCAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGGGAGCCTATG
 TTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGGACTCCCAGC
 TATCAGTATCCCAGCTTACTTATCTGAGTCTGGTTTACCCATAGGGACGA
 TGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAATTTGCAACT
 TTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCAAAGAATAATAGA
 TAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACTAACTCCCTCT
 TTAAGGCTCATTTCATCTAGTAAATTTAGAAGAAAATTCACAAGTTACT
 CAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAAC
 ATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4804

STRAIN COH1

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAAT
 ACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGA
 ATCAGGACAATCTGTAATAGGTCAAGTAAAACAGCTAATTTCTGCGGCGC
 TTACAACAGTTGACACGCTCATATTTAGCTCCAGATGCTTTAAAAACA
 ACTCAATCAAGTCCTGTGCTTGAGAGTCTTTCTACTAAGTTAACTGAAGA
 GACATACAAACAAAAAGATGGTCAAGATTTAGCCAACATGGTGAGAAGTG
 GTCAAGTTACTAGTGAGGAACCTCGTCAATATGGCATAACGATATTATCGCT
 AAAGAAAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGC
 CATTGAAGAGGCTAGAAAACTTAAAGATACCTAATCAGCCGTTTTTAGGTG
 TTCCCTTGTAGTCAAGGGGTTAGGGGCACAGTATTAAAGGTGGTGAAACC
 AATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAG
 CTATGTTCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACAAACGA
 ATTTTCCAGAGTATGGGTGGCGTAATATAACAGACTCTAAATTATACGGT
 CCAACGCATAATCCTTGGAACTTTGCTCATAACGCTGGTGGCTCTTCTGG
 TGGAAAGTGACAGCTATTGCTAGCGGAATGACGCCAATTTGCTAGCGGCA
 GTGATGCTGGTGGTTCTATCCGTATTCATCTTCTTGGACGGGCTTAGTA
 GGTTTAAACCAACAAGAGGATTTGGTGAGTAATGAAAAGCCAGATTTCGTA
 TAGTACAGCAGTTTCATTTTCCATTAACTAAGTCATCTAGAGACGCAGAAA
 CATTGTTAACTTACCTAAAGAAAAGCGATCAAACGCTAGTATCAGTTAAT
 GATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAAC
 AGAAGTTAGTCAAGATGCTAAAAATGCTATTATGGACAACGTCACATTCT
 TAAGAAAACAAGGATTCAAAGTGACAGAGATAGATTACCAATTGATGGT
 AGAGCATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGC
 TTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTACTAAAGAAG
 ACGTTGATCCCATTACTTGGGCAGTTTCATGTTATTATCAAAATTAGAT
 AAGGCTGAACCTTAAGAAATCTATTGTGGAAGCCCAAAACATATGGATGA
 TTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTATTTTCTTAT
 CGCCAACGACCGCAAGTTTAGCCCCCTCTAAATACAGATCCATATGTAACA
 GAGAAAGATAAAAGAGCGATTATAATATGGAAAACTTGAGCCAAGAAGA
 AAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACAC
 CTTTTACACCAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCG
 ACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGG
 TGCAAACTATGATATGGTATTAAATTAAATTGCAACTTTCTTTGAAAAAC
 ATCATGGTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAA
 CCATCTGCTGACCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATT
 ATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCT
 CTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCA
 TATCAAAAAGCA

SEQ ID NO: 4805

STRAIN M732

TCAGTAGCTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCC

Table 48: Comparative Sequences relating to SAG1474

TACCGCAAAATTTGCATCAGAATCAGGACAATCTGTAATAGGTCAAGTAA
 AACCAGCTAATTCTGCGGCGCTTACAACAGTTGACACGCCCTCATATTTCA
 GCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGAGTCC
 TTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGATT
 TAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCAAT
 ATGGCATAAGATATTATCGCTAAAGAAAAACCCATCTTTAAATGCAGTCAT
 TACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAAGATA
 CTAATCAGCCGTTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCAC
 AGTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAA
 AATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGAT
 TTATTATTTTAGGACAAACGAAATTTTCCAGAGTATGGGTGGCGTAATATA
 ACAGACTCTAAATTATACGGTCAACGCATAATCCITGGGATCTTGCTCA
 TAACGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGCTATTGCTAGCGGAA
 TGACGCCAATTGCTAGCGGCAGTGATGCTGGTGGTTCTATCCGTATTCCA
 TCTTCTTGGACGGGCTTAGTAGGTTTAAACCAACAAGAGGATTTGGTGAG
 TAATGAAAAGCCAGATTCGTATAGTACAGCAGTTTCAATTTCCATTAACTA
 AGTCATCTAGAGACGCAGAAACATTGTTAACTTACCTAAAGAAAAGCGAT
 CAAACGCTAGTATCAGTTAATGATTTAAATCTTTACCAATTGCTTATAC
 TTTGAAATCACCATTGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGCTA
 TTATGGACAACGTCACATTTCTTAAGAAAACAAGGATTCAAAGTGACAGAG
 ATAGATTTACCAATTGATGGTAGAGCAITTAATGCGTGATTATTCAACCTT
 GGCTATTGGCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAAA
 AACATGGTTTTACTAAAGAAGACGTTGATCCCATTTACTTGGGCAGTTTAT
 GTTATTTATCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTGTGGA
 AGCCCAAAACATATGGATGATTTATCGTAAGGCAATGGAGAAGCTTCA
 AGCAATTTCTATTTTCTTATCGCCAAACGACCGCAAGTTTAGCCCCCTCTA
 AATACAGATCCATATGTTACAGAGAAAGATAAAAGAGCGATTATAATAT
 GGAAAACTTGAGCCAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGGG
 AGCCTATGTTGCGTAGAACACCTTTTACACCAATTGCTAATATGACAGGA
 CTCCAGCTATCAGTATCCCGACTTACTTTATCTGAGTCTGGTTTACCCAT
 AGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAAT
 TTGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGA
 ATAATAGATAAAGAAAGTGAAACCATCTGCTGACCTAATACAGCCTACTAA
 CTCCCTCTTTAAAGCTCATTTCATCATTAGTAAATTTAGAAGAAAATTCAC
 AAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAA
 AATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4806

STRAIN 18RS21

AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAAATACTATCGT
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCAGAATCAGGAC
 AATCTGTAATAGGTCAAGTAAAACCAAGATAATTTCTGCGGCGCTTACAACA
 GTTGACACGCCCTCATCATATTTAGCTCCAGATGCTTTAAAAACAACCTCA
 ATCAAGTCCGTGCTGTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACTT
 ACAAACAAAAAGATGGTCAAGATTTAGCCAACATGGTGAGAAGTGGTCAA
 GTTACTAGTGAGGAACTCGTTAATATGGCATAACGATATTATTGCTAAAGA
 AAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCTATTG
 AAGAGGCTAGAAAACCTTAAAGATACCAATCAGCCGTTTTTTAGGTGTTCCC
 TTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAAACCAATAA
 TGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAGCTATG
 TCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACAAACGAACTTT
 CCAGAGTATGGGTGGCGTAATATAACAGATTTCTAAATTTATACGGTCTAAC
 GCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGGAA
 GTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAGCGGTAGTGAT
 GCTGGTGGTTCTATCCGTATTCCATCTTCTTGGACGGGCTTGGTAGGTTT
 AAAACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGATTCGTATAGTA
 CAGCAGTTCAATTTCCATTAACTAAGTCATCTAGAGACGCAGAAACATTA
 TTAACCTATCTAAAGAAAAGCGATCAAACGCTAGTATCAGTTAATGATTT
 AAAATCTTTACCAATTGCTTATACCTTTGAAATCACCATTGGGAACAGAAG
 TTAGTCAAGATGCTAAAAACGCTATTATGGACAACGTCACATTTCTTAAGA
 AAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGC
 ATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTTT
 CAACAATTGAAAAAGACTTAAAAAAACATGGTTTTTACTAAAGAAGACGTT
 GATCCTATTACTTGGGCAGTTTATGTTATTTATCAAAATTCAGATAAGGC
 TGAACCTAAGAAATCTATTATGGAAGCCCAAAACATATGGATGATTATC
 GTAAGGCAATGGAGAAGCTTCAAGCAATTTCCATTTTCTTATCGCCA
 ACGACCGCAAGTTTAGCCCCCTCTAAATACAGATCCATATGTAACAGAGGA
 AGATAAAAGAGCGATTATAATATGGAAAACCTTGAGCCAAGAAGAAAGAA
 TTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTT
 ACACAAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCGACTTA
 CTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAA
 ACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAAACATCAT
 GGTTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAACCATC
 TACTGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTTCATCAT
 TAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTCTAAA
 AATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCA
 AAAAGCA

SEQ ID NO: 4807

STRAIN M781

TGCTTCAGTAGCTCCTACTACAAATACTATCGTTCAAACTAATGACAGTA
 ATCCTACCGCAAAATTTGCATCAGAATCAGGACAATCTGTAATAGGTCAA
 GTAAAACCAGCTAATTTCTGCGGCGCTTACAACAGTTGACACGCCCTCATAT

Table 48: Comparative Sequences relating to SAG1474

TTCAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGA
 GTCCTTCTACTAAGTTAACTGAAGAGACATACAAAACAAAAGATGGTCAA
 GATTTAGCCAAACATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACCTCGT
 CAATATGGCATTACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAG
 TCATTACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAA
 GATACTAATCAGCCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGG
 GCACAGTATtAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATG
 GAAAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTAA
 GGATTTATTATTTTAGGACAAACGaATTTTCCAGAGTATGGGTGGCGTAA
 TATAACAGACTCTAAATTATACGGTCCAACGCATAATCCTTGGAaTCTTG
 CTCATAACGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGCTATTGCTAGC
 GGAATGACGCCAATTGCTAGCGGCAGTGATGCTGGTGGTTCTATCCGTAT
 TCCATCTTCTTTGGACGGGCTTAGTAGGTTTAAAAACCAACAAGAGGATTGG
 TGAGTAATGAAAAGCCAGATTTCGTATAGTACAGCAGTTCATTTTCCATTA
 ACTAAGTCATCTAGAGACGCAGAAACATTGTTAACTTACCTAAAGAAAAG
 CGATCAAACGCTAGTATCAGTTAATGATTAAAAaTCTTTACCAATTGCTT
 ATACTTTGAAATCACCAATGGGAACAGAAgTTAGTCAAGATGCTAAAAAT
 GCTATTATGGACAACCTCACATTTCTTAAGAGAACCAAGGATTCAAAGTGAC
 AGAGATAGATTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCAA
 CCTTGGCTATTGGCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTA
 AAAAAACATGGTTTTTACTAAAGAAAGACGTTGATCCCATTACTTTGGGCAGT
 TCATGTTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTG
 TGGAAGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTT
 CACAAGCAATTTCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCC
 TCTAAATACAGATCCATATGTAACAGaGaAGATAAAAGAGCGATTATA
 ATATGGAAAACCTTGAGCCAAGAAAGAAAGAAATTGCTCTCTTTAATCGCCAG
 TGGGAGCCTATGTTGCGTAGAACACCTTTTACACCAATTGCTAATatGAC
 AGGACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTAC
 CCATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAAT
 AAATTTGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCA
 AAGAATAATAGATAAAGAAAGTGAAACCATCTGCTGACCTAATACAGCCTA
 CTAACCTCCCTCTTTAAAGCTCAFTCATCATTTAGTAAATTTAGAAGAAAAT
 TCACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGT
 TAAAAATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4810

STRAIN CJB110

TAGTTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACC
 GCAAAATTTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAAACC
 AGATAATTTCTGCGGCGCTTACAACAGTTGACACGCCCTCATCATATTTAG
 CTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGAGTACT
 CTACTAAGTTAACTGAAGAGACTTACAAACAAAAGATGGTAAAGATT
 AGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATA
 TGGCATAACGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATT
 ACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATAC
 CAATCAGCCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCACA
 GTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATGGAAAA
 ATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGATT
 TATTATTTTAGGACAAACGAACCTTTCCAGAGTATGGGTGGCGTAATATAA
 CAGATTCTAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCAT
 AATGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGCCATTGCTAGCGGAAT
 GACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCCAT
 CTTCTTGGACGGGCTTGGTAGGTTTTAAAAACCAACAAGAGATTTGGTGAGT
 CATGAAAAGCCAGATTTCGTATAGTACAGCAGTTCATTTTCCATTAACTAA
 GTCATCTAGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAAGCGATC
 AAACGCTAGTATCAGTTAATGATTTAAATCTTTTACCAATTGCTTATACT
 TTGAAATCACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAACGCTAT
 TATGGACAACGTCACATTTCTTAAGAAAACAAGGATTCAAAGTAAACAGAGA
 TAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCAACCTTG
 GCTATTGGCATGGGA_gGAGCTTTTTCAACaATTGAAAAAGAcTTAaAAAA
 AcATGGTTTTACTAAAGAAGACGTTGATCCTATTACTTTGGGCAGTTTCATG
 TTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAA
 GCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAA
 GCAATTTCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCCTCTAA
 ATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTTATAATATG
 GAAAACCTTGAGCCAAGAAGAAAGAAATTGCTCTCTTTAATCGCCAGTGGGA
 GCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATAatGACAGGAC
 TCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATA
 gGGACgATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAATTT
 TGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAGAA
 TAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACTAAC
 TCCCTCTTTAAAGCTCAFTCATCATTTAGTAAATTTAGAAGAAAATTCACA
 AGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTAAAA
 ATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4811

STRAIN 1169NT

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAATACTATCGT
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGCATCAGAATCAGGAC
 AATCTGTAATATGTCAAGTAAAACAGATAAATCTGCGGCGCTTACAACA
 GTTGACACGCCCTCATATTTAGCTCCAGATGATTAAAAACAACCTCAATC
 AAGTCTGTGCTGAGAGTACTTCTACTAAGTTAACTGAAGAGACATACA
 AACAAAAGATGGTCAAGATTTAGCCAACATGGTGAGAAGTGGTCAAGTT

Table 48: Comparative Sequences relating to SAG1474

ACTAGTGAGGAACTCGTCAATATGGCATACGATATTATTGCTAAAGAAAA
 CCCTTCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCCATTGAAG
 AGGCTAGAAAACTTAAAGATACTAATCAGCCATTTTATAGGTGTTCCCTTG
 TTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAACCAATAATGG
 CTTGATCTATGCAGATGGAAAAATtAGCACATTTGACAGTAGCTATGTCA
 AAAAATATAAAGATTTAGGATTTATTATTTTAGGACAAACGAACTTTCCA
 GAGTATGGGTGGCGTAATATAACAGATTCTAAATTATACGGTCCAACGCA
 TAACCTTCGGAATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGGAAAGTG
 CAGCAGCCATTGCTAGCGGATGACGCCAATTGCTAGCGGTAGTGATGCT
 GGTGGTTCTATCCGtATTCCATCTTCTGGACGGGCTTGGTAGGTTTAAA
 ACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGATTCTGTATAGTACAG
 CAGTTTCATTTTCCATTAACTAAGTCATCTAGAGACGCAGAAACATTATTA
 ACTTATCTAAAGAAAAGCGATCAAAACGCTAGTATCAGTTAATGATTTAAA
 ATCTTTACCAATTGCTTATACCTTTGAAATCACCAATGGGAACAGAAGTTA
 GTCAAGATGCTAAAAACGCTATTATGGACAACGTCACATTCTTAAGAAAA
 CAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGCATT
 AATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTTCAA
 CAATTGAAAAAGACTTAAAAAACATGGTTTACTAAAGAAGACGTTGAT
 CCTATTACTTGGGCAGTTTATGTTATTATCAAAATTCAGATAAGGCTGA
 ACTTAAGAAATCTATTATGGAAGCCCAAAACATATGGATGATTATCGTA
 AGGCAATGGAGAAGCTTCAAGCAATTTCTATTTTCTTATCGCCAACG
 ACCGCAAGTTTAGCCCTCTAAATACAGAtCCATATGTAACAGAGGAAGA
 TAAAAGAGCGATTATATAATATGGAAAACTTGAGCCAAGAAGAAAGATTG
 CTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTTACA
 CAAATTGCTAATATGACAGGACTCCAGCTATCAGTATCCCGACTTACTT
 ATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAAACT
 ATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAAACATCATGGT
 TTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAACCATCTAC
 TGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCATTAG
 TAAATTTAGAAGAAATTCACAAGTTACTCAAGTATCTATCTCTAAAAAA
 TGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCAAAA
 AGCA

SEQ ID NO: 4812

STRAIN JM9130013

TTTCAGTAGCTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATC
 CTACCGCAAAATTTTCATCAGAATCAGGACAATCTGTAATAGGTCAAGTA
 AAACCAGCTAATTCTGTGGCGCTTACAACAGTTGACACGCCCTCATATTTT
 AGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTTGAGAGTC
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGAG
 TTAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCAA
 TATGGCATAAGCATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCA
 TTAATACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGAT
 ACCAATCAGCCGTTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCA
 CAGTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGGTGGAA
 AAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGA
 TTTTATTATTTTAGGACAAACGAACCTTTCCAGAGTATGGATGGCGCAATAT
 AACAGATTCTAAATTATACGGTCCAACGCATAACCCCTGGAAATCTTGCTC
 ATAATGCTGGTGGCTCTTCTGGTGGAAAGTGCAGCAGTTATTGCTAGCGGG
 ATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCC
 ATCTTCTGGACGGGCTTGGTAGGTTTAAACCAACAAGAGGATTGGTGA
 GTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCAATTTCCATTAACT
 AAGTCATCTAGAGACGCAGAAAACATTATTAACCTTATCTAAAGAAAAGCGA
 TCAAACGCTAGTATCAGTTAATGATTTAAATCTTTACCAATTGCTTATA
 CTTTGAAATCACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAATGCT
 ATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAGA
 GATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCAACCT
 TGGCTATTGGTATGGGAGGAGCTTTTTCAACAATTGAAAAGACTTAAAA
 AAACATGGTTTTACTAAAGAAAGACGTTGATCCCATTTCTGGGGAGTTCA
 TGTTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGG
 AAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCAC
 AAGCAATTTCTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCT
 AAATACAGATCCATATGTAAACAGAGGAAGATAAAAGAGCGATTATATAATA
 TGGAAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGG
 GAGCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGG
 ACTCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCA
 TAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATAAA
 TTTGCAACTTTCTTTGAAAAATATCATGGTTTTAATGTTAAATGGCAAAG
 AATAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACTA
 ACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTC
 CAAGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGTAA
 AAATAAACCATCCGTAATGGCATAT

SEQ ID NO: 4813

STRAIN H36B

CTTCAGTAGTTCCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAAT
 CCTACCGCAAAATTTTCATCAGAATCAGGACAATCTGTAATAGGTCAAGT
 AAAACCAGCTAATTCTGTGGCGCTTACAACAGTTGACACGCCCTCATATTT
 CAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTTGAGAGT
 CCTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGA
 TTTAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCA
 ATATGGCATaCGATAtTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCT
 ATTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGA

Table 48: Comparative Sequences relating to SAG1474

TACCAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGC					
ACAGTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGGTGGA					
AAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGG					
ATTTATTATTTTAGGACAAACGAACTTTCCAGAGTATGGATGGCGCAATA					
TAACAGATTCTAAATTATACGGTCCAACGCATAACCCTTGGAATCTTGCT					
CATAATGCTGGTGGCTCTTCTGGTGGAGTGCAGCAGTTATTGCTAGCGG					
GATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTC					
CATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAAGAGGATTGGTG					
AGTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTTCAATTTCCATTAA					
TAAGTCATCTAGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAAGCG					
ATCAAACGCTAGTATCAGTTAATGATTTAAATCTTTACCAATTGCTTAT					
ACTTTGAAATCACCATTGGGAACAGAAGTTAGTCAAGATGCTAAAAATGC					
TATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAG					
AGATAGACTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACC					
TTGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTAAA					
AAAACATGGTTTTTACTAAAGAAGACGTTGATCCCATTAATTGGGCAGTTC					
ATGTTATTTTATCAAAATTCAGATAAGGCTGAACCTAAGAAATCTATTATG					
GAAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCA					
CAAGCAATTTCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCTC					
TAAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATATAAT					
ATGGAAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTAAATCGCCAGTG					
GGAGCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAG					
GACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCC					
ATAGGGACGATGTTAATGGCAGGTGCAACTATGATATGGTATTAATTAA					
ATTTGCAACTTTCTTTGAAAAATATCATGGTTTTAATGTTAAATGGCAAA					
GAATAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACT					
AACTCCCTCTTTAAAGCTCATTTCATCATTAGTAAATTTAGAAGAAAATTC					
ACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTA					
AAAATAAA					
PRETTY of: /biotmp/msa71927.2{*} January 22, 2003 07:23 ..					
1					
msa71927.2{173_18RS21}	aatagtactg	agacaagtgc	ttcagtagtt	ccTACTACAA	ATACTATCGT
msa71927.2{173_2603}	aatagtactg	agacaagtgc	ttcagtagtt	ccTACTACAA	ATACTATCGT
msa71927.2{173_A909}	-----	-----	-----	---TACTACAA	ATACTATCGT
msa71927.2{173_090}	aatagtactg	agacaagtgc	ttcagtagtt	ccTACTACAA	ATACTATCGT
msa71927.2{173_CJB110}	-----	-----	-----tagtt	ccTACTACAA	ATACTATCGT
msa71927.2{173_COH1}	aatagtactg	agacaagtgc	ttcagtagct	ccTACTACAA	ATACTATCGT
msa71927.2{173_M781}	-----	-----tgc	ttcagtagct	ccTACTACAA	ATACTATCGT
msa71927.2{173_M732}	-----	-----	-tcagtagct	ccTACTACAA	ATACTATCGT
msa71927.2{173_H36B}	-----	-----c	ttcagtagtt	ccTACTACAA	ATACTATCGT
msa71927.2{173_JM9130013}	-----	-----	ttcagtagct	ccTACTACAA	ATACTATCGT
msa71927.2{173_1169NT}	aatagtactg	agacaagtgc	ttcagtagct	ccTACTACAA	ATACTATCGT
Consensus	-----	-----	-----	*****	*****
51					
msa71927.2{173_18RS21}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgtATCA	GAATCAGGAC
msa71927.2{173_2603}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgtATCA	GAATCAGGAC
msa71927.2{173_A909}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgtATCA	GAATCAGGAC
msa71927.2{173_090}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgtATCA	GAATCAGGAC
msa71927.2{173_CJB110}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgtATCA	GAATCAGGAC
msa71927.2{173_COH1}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgcATCA	GAATCAGGAC
msa71927.2{173_M781}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgcATCA	GAATCAGGAC
msa71927.2{173_M732}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgcATCA	GAATCAGGAC
msa71927.2{173_H36B}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTtcATCA	GAATCAGGAC
msa71927.2{173_JM9130013}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTtcATCA	GAATCAGGAC
msa71927.2{173_1169NT}	TCAAACCTAAT	GACAGTAATC	CTACCGCAAA	ATTTgcATCA	GAATCAGGAC
Consensus	*****	*****	*****	****_****	*****
101					
msa71927.2{173_18RS21}	AATCTGTAAT	AgGTCAAGTA	AAACCAGaTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_2603}	AATCTGTAAT	AgGTCAAGTA	AAACCAGaTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_A909}	AATCTGTAAT	AgGTCAAGTA	AAACCAGaTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_090}	AATCTGTAAT	AgGTCAAGTA	AAACCAGaTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_CJB110}	AATCTGTAAT	AgGTCAAGTA	AAACCAGaTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_COH1}	AATCTGTAAT	AgGTCAAGTA	AAACCAGcTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_M781}	AATCTGTAAT	AgGTCAAGTA	AAACCAGcTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_M732}	AATCTGTAAT	AgGTCAAGTA	AAACCAGcTA	ATTCTGcGGC	GCTTACAACA
msa71927.2{173_H36B}	AATCTGTAAT	AgGTCAAGTA	AAACCAGcTA	ATTCTGtGGC	GCTTACAACA
msa71927.2{173_JM9130013}	AATCTGTAAT	AgGTCAAGTA	AAACCAGcTA	ATTCTGtGGC	GCTTACAACA
msa71927.2{173_1169NT}	AATCTGTAAT	AtGTCAAGTA	AAACCAGaTA	ATTCTGcGGC	GCTTACAACA
Consensus	*****	*_*****	*****_**	*****_***	*****
151					
msa71927.2{173_18RS21}	GTTGACACGC	CtcaTCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_2603}	GTTGACACGC	CtcaTCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_A909}	GTTGACACGC	CtcaTCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_090}	GTTGACACGC	CtcaTCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_CJB110}	GTTGACACGC	CtcaTCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_COH1}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_M781}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_M732}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
200					

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_H36B}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_JM9130013}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_1169NT}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGaTTTAA	AAACAACCTCA
Consensus	*****	*--*****	*****	****-*****	*****
201					
msa71927.2{173_18RS21}	ATCAAGTCCT	GTCGTTGAGA	GTaCTTCTAC	TAAGTTAACT	GAAGAGACTT
msa71927.2{173_2603}	ATCAAGTCCT	GTCGTTGAGA	GTaCTTCTAC	TAAGTTAACT	GAAGAGACTT
msa71927.2{173_A909}	ATCAAGTCCT	GTCGTTGAGA	GTaCTTCTAC	TAAGTTAACT	GAAGAGACTT
msa71927.2{173_090}	ATCAAGTCCT	GTCGTTGAGA	GTaCTTCTAC	TAAGTTAACT	GAAGAGACTT
msa71927.2{173_CJB110}	ATCAAGTCCT	GTCGTTGAGA	GTaCTTCTAC	TAAGTTAACT	GAAGAGACTT
msa71927.2{173_COH1}	ATCAAGTCCT	GTCGTTGAGA	GTcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_M781}	ATCAAGTCCT	GTCGTTGAGA	GTcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_M732}	ATCAAGTCCT	GTCGTTGAGA	GTcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_H36B}	ATCAAGTCCT	GTCGTTGAGA	GTcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_JM9130013}	ATCAAGTCCT	GTCGTTGAGA	GTcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_1169NT}	ATCAAGTCCT	GTCGTTGAGA	GTaCTTCTAC	TAAGTTAACT	GAAGAGACaT
Consensus	*****	*****	**-*****	*****	*****-
251					
msa71927.2{173_18RS21}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_2603}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_A909}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_090}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_CJB110}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_COH1}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M781}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M732}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_H36B}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_JM9130013}	ACAAACAAAA	AGATGGTcAA	GAGTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_1169NT}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
Consensus	*****	*****-	**-*****	*****	*****
301					
msa71927.2{173_18RS21}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_2603}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_A909}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_090}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_CJB110}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_COH1}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_M781}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_M732}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_H36B}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_JM9130013}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_1169NT}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
Consensus	*****	*****	-*****	*****	*-*****
351					
msa71927.2{173_18RS21}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_2603}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_A909}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_090}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_CJB110}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_COH1}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_M781}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_M732}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_H36B}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_JM9130013}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_1169NT}	AAACCCtTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
Consensus	*****-	*****	*****	*****	*****-
401					
msa71927.2{173_18RS21}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_2603}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_A909}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_090}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_CJB110}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_COH1}	AAGAGGCTAG	AAAACCTTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M781}	AAGAGGCTAG	AAAACCTTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M732}	AAGAGGCTAG	AAAACCTTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_H36B}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_JM9130013}	AAGAGGCTAG	AAAACCTTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_1169NT}	AAGAGGCTAG	AAAACCTTAAA	GATACtAATC	AGCCaTTTTT	AGGTGTTCCC
Consensus	*****	*****	*****-	*****	*****
451					
msa71927.2{173_18RS21}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_2603}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_A909}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_090}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_CJB110}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_COH1}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_M781}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M732}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_H36B}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_JM9130013}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_1169NT}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
Consensus	*****	*****	*****	*****	*****
501					
msa71927.2{173_18RS21}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_2603}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_A909}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_090}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_CJB110}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_COH1}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M781}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M732}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_H36B}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_JM9130013}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_1169NT}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
Consensus	*****	*****	*****	*****	*****
551					
msa71927.2{173_18RS21}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_2603}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_A909}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_090}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_CJB110}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_COH1}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_M781}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_M732}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_H36B}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_JM9130013}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_1169NT}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
Consensus	*****	*****	*****	*****	*****
601					
msa71927.2{173_18RS21}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_2603}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_A909}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_090}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_CJB110}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_COH1}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAc	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_M781}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAc	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_M732}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAc	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_H36B}	CCAGAGTATG	GaTGGCGcAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_JM9130013}	CCAGAGTATG	GaTGGCGcAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
msa71927.2{173_1169NT}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAt	TCTAAATTAT	ACGGTcAAC
Consensus	*****	*-*****	*****	*****	*****
651					
msa71927.2{173_18RS21}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_2603}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_A909}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_090}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_CJB110}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_COH1}	GCATAAcCCT	tGGgATCTTG	CTCATAAcGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M781}	GCATAAcCCT	tGGgATCTTG	CTCATAAcGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M732}	GCATAAcCCT	tGGgATCTTG	CTCATAAcGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_H36B}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_JM9130013}	GCATAAcCCT	tGGgATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_1169NT}	GCATAAcCCT	cGGaATCTTG	CTCATAAtGC	TGGTGGCTCT	TCTGGTGGAA
Consensus	*****	-*-*****	*****	*****	*****
701					
msa71927.2{173_18RS21}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_2603}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_A909}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_090}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_CJB110}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_COH1}	GTGCAGCAGc	tATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGcAGTGAT
msa71927.2{173_M781}	GTGCAGCAGc	tATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGcAGTGAT
msa71927.2{173_M732}	GTGCAGCAGc	tATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGcAGTGAT
msa71927.2{173_H36B}	GTGCAGCAGt	tATTGCTAGC	GGgATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_JM9130013}	GTGCAGCAGt	tATTGCTAGC	GGgATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_1169NT}	GTGCAGCAGc	cATTGCTAGC	GGrATGACGC	CAATTGCTAG	CGGtAGTGAT
Consensus	*****	-*****	*****	*****	*****
751					
msa71927.2{173_18RS21}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_2603}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_A909}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_090}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_CJB110}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_COH1}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TagTAGGTTT

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M781}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_M732}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_H36B}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_JM9130013}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_1169NT}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
Consensus	*****	*****	*****	*****	*_*****
801					
msa71927.2{173_18RS21}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_2603}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_A909}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_090}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_CJB110}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_COH1}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M781}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M732}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_H36B}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_JM9130013}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_1169NT}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
Consensus	*****	*****	*****	*****	*****
851					
msa71927.2{173_18RS21}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_2603}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_A909}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_090}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_CJB110}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_COH1}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M781}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M732}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_H36B}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_JM9130013}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_1169NT}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
Consensus	*****	*****	*****	*****	*****
901					
msa71927.2{173_18RS21}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_2603}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_A909}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_090}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_CJB110}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_COH1}	TTAACTTAcC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_M781}	TTAACTTAcC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_M732}	TTAACTTAcC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_H36B}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_JM9130013}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_1169NT}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
Consensus	*****	*****	*****	*****	*****
951					
msa71927.2{173_18RS21}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_2603}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_A909}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_090}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_CJB110}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_COH1}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_M781}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_M732}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_H36B}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_JM9130013}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
msa71927.2{173_1169NT}	AAAATCTTTA	CCAATTGCTT	ATACTTTGAA	ATCACCAATG	GGAACAGAAG
Consensus	*****	*****	*****	*****	*****
1001					
msa71927.2{173_18RS21}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_2603}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_A909}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_090}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_CJB110}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_COH1}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_M781}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_M732}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_H36B}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_JM9130013}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
msa71927.2{173_1169NT}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCAc	ATTCTTAAGA
Consensus	*****	*****	*****	*****	*****
1051					
msa71927.2{173_18RS21}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_2603}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_A909}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_090}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_CJB110}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_COH1}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAt	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_M781}	gAACAAGGAT	TCAAAGTgAC	AGAGATAGAt	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_M732}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAt	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_H36B}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_JM9130013}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_1169NT}	aaACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
Consensus	*****	*****-*	*****-	*****	*****
msa71927.2{173_18RS21}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_2603}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_A909}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_090}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_CJB110}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_COH1}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M781}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M732}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_H36B}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_JM9130013}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_1169NT}	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
Consensus	*****	*****	*****	***-*****	*****
msa71927.2{173_18RS21}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_2603}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_A909}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_090}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_CJB110}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_COH1}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M781}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M732}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_H36B}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_JM9130013}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_1169NT}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_2603}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_A909}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_090}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_CJB110}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_COH1}	GATCCcATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M781}	GATCCcATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M732}	GATCCcATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_H36B}	GATCCcATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_JM9130013}	GATCCcATTA	CTTGGGgAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
msa71927.2{173_1169NT}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAATT	CAGATAAGGC
Consensus	*****	*****-***	*****	*****	*****
msa71927.2{173_18RS21}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_2603}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_A909}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_090}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_CJB110}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_COH1}	TGAACCTAAG	AAATCTATTg	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_M781}	TGAACCTAAG	AAATCTATTg	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_M732}	TGAACCTAAG	AAATCTATTg	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_H36B}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_JM9130013}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_1169NT}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
Consensus	*****	*****-	*****	*****	*****
msa71927.2{173_18RS21}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_2603}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_A909}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_090}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_CJB110}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_COH1}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_M781}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_M732}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_H36B}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_JM9130013}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
msa71927.2{173_1169NT}	GTAAGGCAAT	GGAGAAGCTT	CACAAGCAAT	TTCTATTTT	CTTATCGCCA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_2603}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_A909}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_090}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_CJB110}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_COH1}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGaA
msa71927.2{173_M781}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGaA
msa71927.2{173_M732}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TtACAGAGaA
msa71927.2{173_H36B}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_JM9130013}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_1169NT}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
Consensus	*****	*****	*****	*****	*-*****
1401					
msa71927.2{173_18RS21}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_2603}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_A909}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_090}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_CJB110}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_COH1}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M781}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M732}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_H36B}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_JM9130013}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_1169NT}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
Consensus	*****	*****	*****	*****	*****
1451					
msa71927.2{173_18RS21}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_2603}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_A909}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_090}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_CJB110}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_COH1}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M781}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M732}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_H36B}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_JM9130013}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_1169NT}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
Consensus	*****	*****	*****	*****	*****
1501					
msa71927.2{173_18RS21}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_2603}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_A909}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_090}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_CJB110}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_COH1}	ACACcAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M781}	ACACcAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M732}	ACACcAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_H36B}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_JM9130013}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_1169NT}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
Consensus	****-*****	*****	*****	*****	*****
1551					
msa71927.2{173_18RS21}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_2603}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_A909}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_090}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_CJB110}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_COH1}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M781}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M732}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_H36B}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_JM9130013}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_1169NT}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
Consensus	*****	*****	*****	*****	*****
1601					
msa71927.2{173_18RS21}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_2603}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_A909}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_090}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_CJB110}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_COH1}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_M781}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_M732}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_H36B}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_JM9130013}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
msa71927.2{173_1169NT}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAAcATCAT
Consensus	*****	*****	*****	*****	****-*****
1651					
msa71927.2{173_18RS21}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_2603}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_A909}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_090}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_CJB110}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_COH1}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M781}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M732}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_H36B}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_JM9130013}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_1169NT}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
Consensus	*****	*****	*****	*****	*****
1701					
msa71927.2{173_18RS21}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_2603}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_A909}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_090}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_CJB110}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_COH1}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_M781}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_M732}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_H36B}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_JM9130013}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
msa71927.2{173_1169NT}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTCATCAT
Consensus	*-***-****	*****	*****	*****	*****
1751					
msa71927.2{173_18RS21}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_2603}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_A909}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_090}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_CJB110}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_COH1}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_M781}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_M732}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_H36B}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_JM9130013}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_1169NT}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
Consensus	*****	*****	*****	*****	*****
1801					
msa71927.2{173_18RS21}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_2603}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_A909}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_090}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_CJB110}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_COH1}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_M781}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_M732}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_H36B}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	-----	-----
msa71927.2{173_JM9130013}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatat--
msa71927.2{173_1169NT}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
Consensus	*****	*****	*****	-----	-----
1851					
msa71927.2{173_18RS21}	aaaagca				
msa71927.2{173_2603}	aaaagca				
msa71927.2{173_A909}	aaaagca				
msa71927.2{173_090}	aaaagca				
msa71927.2{173_CJB110}	aaaagca				
msa71927.2{173_COH1}	aaaagca				
msa71927.2{173_M781}	aaaagca				
msa71927.2{173_M732}	aaaagca				
msa71927.2{173_H36B}	-----				
msa71927.2{173_JM9130013}	-----				
msa71927.2{173_1169NT}	aaaagca				
Consensus	-----				

SEQ ID NO: 4814

STRAIN 2603 frame: 1

NSTETSASVVPTINTIVQTNDNPTAKFVSESGQSVIGQVKPDNSAALTTVDPHHISAP
 DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAVDIIAKENPS
 LNAVITTRRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGETNNGLIYADGKISTFD
 SSVVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSAAAIAS
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSPKSDSYSTAVHFPLTKSSRDAETL
 LTYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFQVTEID
 LPIDGRALMRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELK
 KSIMEAQKHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
 EERIALFNQWEPMLRRTFPTQIANMTGLPAISIPTYLSESGLPITMLMAGANYDMVLI
 KFATFFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISK
 KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4815

STRAIN_090 frame: 1

NSTETSASVVPTINTIVQTNDNPTAKFVSESGQSVIGQVKPDNSAALTTVDPHHISAP

Table 48: Comparative Sequences relating to SAG1474

DALKTTQSSPVVESTSTKLTEETYKQKDGKDLANMVRSGQVTSEELVNMAYDIIAKENPS
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLGHSIKGETNNGLIYADGKISTFD
 SSVVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSAAAIAS
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSTAVHFPLTKSSRDAETL
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEID
 LPIDGRALMRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELK
 KSIMEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
 KFATFFEKHGHNFKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSIK
 KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4816

STRAIN A909 frame: 2

TTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPDALKTTQSSPV
 VESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTRRQ
 AIEEARKLKDTNQPFLLVGLGHSIKGETNNGLIYADGKISTFDSSSVVKYKDLG
 FIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSAAAIASGMTPIASGSDA
 GGSIRIPSSWTGLVGLKPTRGLVSNEKPDSTAVHFPLTKSSRDAETLLTYLKKSDQTL
 VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDLPIDGRALMRD
 YSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKHMD
 DYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFNRQW
 EPMRLRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEKHG
 FNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSIKWMKSSVKNK
 SVMAYQKA

SEQ ID NO: 4817

STRAIN COH1 frame: 1

NSTETSASVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSAAALTTVDTPHHISAPD
 ALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSL
 NAVITTRRQEAIEEARKLKDTNQPFLLVGLGHSIKGETNNGLIYADGKISTFDS
 SYVKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSAAAIASG
 MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSTAVHFPLTKSSRDAETLL
 TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDLP
 PIDGRALMRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKK
 SIVEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQE
 ERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK
 FATFFEKHGHNFKWQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSIK
 WMKSSVKNKPSVMAYQKA

SEQ ID NO: 4818

STRAIN M732 frame: 1

SVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSAAALTTVDTPHHISAPDALKTTQ
 SPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTR
 RQEAIEEARKLKDTNQPFLLVGLGHSIKGETNNGLIYADGKISTFDSSSVVKYK
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSAAAIASGMTPIASG
 SDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSTAVHFPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDLPIDGRAL
 MRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQK
 HMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFN
 RQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEK
 HHGHNFKWQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSIKWMKSSSVK
 NKPSVMAYQKA

SEQ ID NO: 4819

STRAIN 18RS21 frame: 1

NSTETSASVAPTNTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAP
 DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPS
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLGHSIKGETNNGLIYADGKISTFD
 SSVVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSAAAIAS
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSTAVHFPLTKSSRDAETL
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEID
 LPIDGRALMRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELK
 KSIMEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
 KFATFFEKHGHNFKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSIK
 KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4820

STRAIN M781 frame: 2

ASVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSAAALTTVDTPHHISAPDALKTTQ
 SSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVIT
 TRRQEAIEEARKLKDTNQPFLLVGLGHSIKGETNNGLIYADGKISTFDSSSVVKY
 KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSAAAIASGMTPIAS
 GSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSTAVHFPLTKSSRDAETLLTYLKK
 SDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDLPIDGRA
 LMRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ
 KHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALF
 NRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFE
 KHGHNFKWQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSIKWMKSSV
 KNKPSVMAYQKA

SEQ ID NO: 4821

STRAIN CJB110 frame: 3

Table 48: Comparative Sequences relating to SAG1474

VPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALT TVDTPHHISAPDALKTTQSS
 PVVESTSTKLTEETKYQKDGKDLANMVRSGQVTSEELVN MAYDI IAKENPSLNAVITTRR
 QEAEIEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDS SYVKKYK
 LGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGSA AAIASGMTPIASGS
 DAGGSIRIPSSWTGLVGLKPTRGLVSHKPD SYSTAVHFPLTKSSRDAETLLTYLKKSDQ
 TLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFVTEIDLPI DGRALM
 RDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKH
 MDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFNR
 QWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK FATFFFEKH
 HGFNVKWQRIIDKEVKPSTGLIQPTNSL FKAHSSLVNLEENSQVTQVSISKW MKSSVK
 KPSVMAYQKA

SEQ ID NO: 4822

STRAIN 1169NT frame: 1

NSTETSASVAPTNTIVQTNDSNPTAKFSESGQSVIGQVKPDNSAALT TVDTPHHISAPD
 DLKTTQSSPVVESTSTKLTEETKYQKDGQDLANMVRSGQVTSEELVN MAYDI IAKENPSL
 NAVITTRRQEAEIEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDS
 SYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPNLAHNAGGSSGSA AAIASG
 MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPD SYSTAVHFPLTKSSRDAETLL
 TYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFVTEIDL
 PIDGRALMRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKK
 SIMEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQE
 ERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK
 FATFFFEKH HGFNVKWQRIIDKEVKPSTGLIQPTNSL FKAHSSLVNLEENSQVTQVSISK
 WKSSVKNKPSVMAYQKA

SEQ ID NO: 4823

STRAIN JM9130013 frame: 2

SVAPTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS
 SPVVESTSTKLTEETKYQKDGQDLANMVRSGQVTSEELVN MAYDI IAKENPSLNAVITTR
 RQEAEIEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYAGGKISTFDS SYVKKYK
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPNWLAHNAGGSSGSA AVIASGMTPIASG
 SDAGGSIRIPSSWTGLVGLKPTRGLVSNKPD SYSTAVHFPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFVTEIDLPI DGRAL
 MRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWGVHVIYQNSDKAELKKSIMEAQK
 HMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFN
 RQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK FATFFFEK
 YHGFNVKWQRIIDKEVKPSTGLIQPTNSL FKAHSSLVNLEENSQVTQVSISKW MKSSVK
 NKPSVMAY

SEQ ID NO: 4824

STRAIN H36B frame: 3

SVVPTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS
 SPVVESTSTKLTEETKYQKDGQDLANMVRSGQVTSEELVN MAYDI IAKENPSLNAVITTR
 RQEAEIEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYAGGKISTFDS SYVKKYK
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPNWLAHNAGGSSGSA AVIASGMTPIASG
 SDAGGSIRIPSSWTGLVGLKPTRGLVSNKPD SYSTAVHFPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFVTEIDLPI DGRAL
 MRDYSTLAIGMGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQK
 HMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFN
 RQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK FATFFFEK
 YHGFNVKWQRIIDKEVKPSTGLIQPTNSL FKAHSSLVNLEENSQVTQVSISKW MKSSVK
 NK

PRETTY of: /biotmp/msa72034.2{*} January 22, 2003 07:25 ..

	1		50
msa72034.2{173_090}	nstetsasvv	PTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_18RS21}	nstetsasvv	PTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_2603}	nstetsasvv	PTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_A909}	-----	-TTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_CJB110}	-----v	PTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_COH1}	nstetsasva	PTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M732}	-----sva	PTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M781}	-----asva	PTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_1169NT}	nstetsasva	PTTNTIVQTN DSNPTAKFaS	ESGQSVicQV KpDnSaALTT
msa72034.2{173_H36B}	-----svv	PTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
msa72034.2{173_JM9130013}	-----sva	PTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
Consensus	-----	*****	*****
	51		100
msa72034.2{173_090}	VDTphHISAP	DaLkTTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_18RS21}	VDTphHISAP	DaLkTTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_2603}	VDTphHISAP	DaLkTTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_A909}	VDTphHISAP	DaLkTTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_CJB110}	VDTphHISAP	DaLkTTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_COH1}	VDt.phISAP	DaLkTTQSSP VVESpSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M732}	VDt.phISAP	DaLkTTQSSP VVESpSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M781}	VDt.phISAP	DaLkTTQSSP VVESpSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_1169NT}	VDt.phISAP	DaLkTTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_H36B}	VDt.phISAP	DaLkTTQSSP VVESpSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_JM9130013}	VDt.phISAP	DaLkTTQSSP VVESpSTKLt	EETyKQKDGq eLANMVRSGQ

Table 48: Comparative Sequences relating to SAG1474

Consensus	***--*****	*-*****	****-*****	*****--	-*****
	101				150
msa72034.2{173_090}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_18RS21}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_2603}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_A909}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_CJB110}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_COH1}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_M732}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_M781}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_1169NT}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_H36B}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
msa72034.2{173_JM9130013}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFGLVP
Consensus	*****	*****	*****	*****	*****
	151				200
msa72034.2{173_090}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_18RS21}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_2603}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_A909}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_CJB110}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_COH1}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_M732}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_M781}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_1169NT}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_H36B}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_JM9130013}	LLVKGLGHSI	KGGETNNGLI	YadGKISTFD	SSYVKKYKDL	GFIILGQTNF
Consensus	*****	*****	***-*****	*****	*****
	201				250
msa72034.2{173_090}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_18RS21}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_2603}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_A909}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_CJB110}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_COH1}	PEYGWRNITD	SKLYGLTHNP	wnLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_M732}	PEYGWRNITD	SKLYGxTHNP	wdLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_M781}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_1169NT}	PEYGWRNITD	SKLYGpTHNP	rnLAHNAGGS	SGGSAAaIAS	GMTPIASGSD
msa72034.2{173_H36B}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAvIAS	GMTPIASGSD
msa72034.2{173_JM9130013}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAvIAS	GMTPIASGSD
Consensus	*****	*****	--*****	*****	*****
	251				300
msa72034.2{173_090}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_18RS21}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_2603}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_A909}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_CJB110}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_COH1}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_M732}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_M781}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_1169NT}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_H36B}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_JM9130013}	AGGSIRIPSS	WTGLVGLKPT	RGLVSneKPD	SYSTAVHFPL	TKSSRDAETL
Consensus	*****	*****	*****	*****	*****
	301				350
msa72034.2{173_090}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_18RS21}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_2603}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_A909}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_CJB110}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_COH1}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_M732}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_M781}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_1169NT}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_H36B}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNViFLR
msa72034.2{173_JM9130013}	LTYLKKSDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSQDAKN	AIMDNViFLR
Consensus	*****	*****	*****	*****	*****
	351				400
msa72034.2{173_090}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_18RS21}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_2603}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_A909}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_CJB110}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_COH1}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_M732}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_M781}	eQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_1169NT}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV
msa72034.2{173_H36B}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV

Table 48: Comparative Sequences relating to SAG1474

msa72034.2{173_JM9130013}	kQGFKVTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
Consensus	*****	*****	*****	*****	*****
	401				450
msa72034.2{173_090}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_18RS21}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_2603}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_A909}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_CJB110}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_COH1}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M732}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M781}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_1169NT}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_H36B}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_JM9130013}	DPITWgVHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
Consensus	*****	*****	*****	*****	*****
	451				500
msa72034.2{173_090}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_18RS21}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_2603}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_A909}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_CJB110}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_COH1}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_M732}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_M781}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_1169NT}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_H36B}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_JM9130013}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
Consensus	*****	*****	*****	*****	*****
	501				550
msa72034.2{173_090}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_18RS21}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_2603}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_A909}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_CJB110}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_COH1}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_M732}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_M781}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_1169NT}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKhH
msa72034.2{173_H36B}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKyH
msa72034.2{173_JM9130013}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFEKyH
Consensus	*..*****	*****	*****	*****	*****
	551				600
msa72034.2{173_090}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_18RS21}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_2603}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_A909}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_CJB110}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_COH1}	GFNVKWQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M732}	GFNVKWQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M781}	GFNVKWQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_1169NT}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_H36B}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_JM9130013}	GFNVKWQRII	DKEVKPStgI	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
Consensus	*****	*****	*****	*****	*****
	601				619
msa72034.2{173_090}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_18RS21}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_2603}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_A909}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_CJB110}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_COH1}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M732}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M781}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_1169NT}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_H36B}	KWMKSSVKNK	-----			
msa72034.2{173_JM9130013}	KWMKSSVKNK	psvmay---			
Consensus	*****	-----			

Table 49: Comparative Sequences related to SAG1502

SEQ ID NO: 4901

STRAIN 2603

aaacatccgataacttaatgatcaaaaatccttagcaattggttgaaacagat
agaatatgatttttgataaattcgataattcagaagcttctttttatgcaa
cattagctagawttcgcgttatggatagagaaatcaaaaatttattaga
gaaaatccaaatagtcaaactcctttcaattgggttggtgacttgatacaag
gtttgaaagagtcgataatggacaaattaggtggtataaccttgatttgc
cagaggttatggagataagaaaattatttttgaagagcatgaaagagtt
actaatatagcaaaatcagccctagatgaaacttggacacgggagggtaaa
tccccaaaatgcccccttttctaactcgtgtcagaaggtgttttaattgtttc
taaaagaagatgacgtagagacttttcttcatatcctgacaaattcattt
agccaatttatggcacaatttgatttgtgtcataaggaaatgattaataa
aggaaagcaacatgatacagtaaaagtatatggatacagaatttcagtttg
gtatcacagatgggtcatgagatttggatttagaccctaaattaaagcaa
ataaatctgatttaactttacagatgagatgagcaaatgtgagttaggcac
acttcgctctttacttccaacaattcgtaaatttaataattgttttaggtg
tgtacgaatataaaagcatc

SEQ ID NO: 4902

STRAIN 090

TAATGATCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTG
ATAAAATTCGATAAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATT
CGCGTTATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAAATAG
TCAAATCCTTTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCG
ATAATGGACAAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAG
ATAAGAAAATTTATTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAA
ATCAGCCATAGATGAACTTGGACACGGGAGGTAAATCCCCAAATGCCC
CTTTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGAC
GTAGAGACTTTTCTTATATCCTGACAAATTCATTTAGCCAATTTATGGC
ACAAATTTGATTTGTGTCTATAAGGAAATGATTAATAAAGGAAAGCAACATG
ATACAGTAAAGTATATGGATACAGAATTTAGTTTGGTATCACAGATGGT
CATGAGATTGTGGATTTAGACCCTAAATTAAGCAAAATAAATCTGATTAA
CTTTACAGATGAGATGAGCAAAATTTAGTTAGGCACACTTCGCTCTTTAC
TTCCAACAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAA
GCATC

SEQ ID NO: 4903

STRAIN A909

AAACATCCGATACCTTAATGA

TCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAAT
TCGATAAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATTTCGCGTT
ATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAAATAGTCAAAT
CCTTTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATG
GACAAATTTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGA
AAATTaTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAAATCAGC
CCTAGATGAACCTTGACACGGGAGGTAAATCCCCAAATGCCCCCTTTTC
TAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGACGTAGAG
ACTTTTCTTATATCCTGACAAATTCATTTAGCCAATTTATGGCACAATT
TGATTTGTGTCTATAAGGAAATGATTAATAAAGGAAAGCAACATGATACAG
TAAAGTATATGGATACAGAATTTAGTTTGGTATCACAGATGGTCATGAG
ATTGTGGATTTAGACCCTAAATTAAGCAAAATAAATCTGATTAACTTTAC
AGATGAGATGAGCAAAATTTAGTTAGGCACACTTCGCTCTTTACTTCCAA
CAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4904

STRAIN H36B

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCA

ATTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAAATTCAGAAGC
TTCTTTTATGCAaCATTAGCTAGAATTTCGCGTTATGGATAGAGAAATCA
AAAAATTTATTAGAGAAAATCCAAATAGTCATATCCTTTCAATTGGCTGT
GgACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTA
TAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAG
AGCATGAAAGAGTTACTAATATAGCAAAAATCAGCCCTAGATGAAACTTGG
ACACGGGAGGTAAATCCCCAAATGCCCCCTTTTCTAATCGTGTGAGAAGG
TGTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTATATCC
TGACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCAgAAG
GAAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATAC
AGAATTTAGTTGGGTATCACAGATGGTCATGAAATTTGTGGATTTAGACC
CTAAATTAAGCAAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAA
TTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAA
TAATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4905

STRAIN 18RS21

AACATCCGATACCTTAATGATCAAAAATCCTTAGCAAT

TGTTGAACAGATAGAATATGATTTTGATAAATTCGATAAATTCAGAAGCTT
CTTTTATGCAACATTAGCTAGAATTTCGCGTTATGGATAGAGAAATCAA
AAATTTATTAGAGAAAATCCAAATAGTCAaATCCTTTCAATTGGTTGTGG
ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA
ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGAG
CATGAAAGAGTTACTAATATAGCAAAAATCAGCCCTAGATGAAACTTGGAC
ACGGGAGGTAAATCCCCAAATGCCCCCTTTTCTAATCGTGTCAgAAGGTG
TTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTATATCCTG

Table 49: Comparative Sequences related to SAG1502

ACAAATTCATTTAGCCAATTTATGGCACaATTTGATTTGTGTCATAaGGA
 AATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG
 AATTTTCAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCCT
 AAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATT
 TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATA
 ATTGTTTAGGTGTGTACGAAtATAaGCATC

SEQ ID NO: 4906

STRAIN M732

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAATTGTTGAACA
 GATAGAATATGATTTGGATAAAATTCGATAATTCAGAAGCTTCTTTTATG
 CAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAAAATTTATT
 AGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTGGACTTGATAC
 AAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATAACCTTGATT
 TGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGAGCATGAAAGA
 GTTACTAATATAGCAAATCAGCCCTAGATGAAACTTGGACACGGGAGGT
 AAATCCCCAAAATGCCCTTTTCTAATCGTGTGAGAAGGTGTTTAATGT
 TTCTAAAAGAGATGACGTAGAGACTTTTCTTCAAtATCCTGACAAATTCA
 TTTAGCCAATTTATGGCaCAATTTGATTTGTGTCATAAGGAAATGATTAA
 TAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAGAATTTAGT
 TTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCCTAAATTAAAG
 CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAgG
 CACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATAATTGTTTAG
 GtGTGTACGAATATAAAGCATC

SEQ ID NO: 4907

STRAIN COH1

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA
 TTGTTGAACAGATAGAATATGATTTGGATAAAATTCGATAATTCAGAAGCT
 TCTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
 AAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTG
 GACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTAT
 AACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGA
 GCATGAAAGAGTTACTAATATAGCAAATCAGCCCTAGATGAAACTTGA
 CACGGGAGGTAAATCCCCAAAATGCCCTTTTCTAATCGTGTGAGAAGGT
 GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCAATCCT
 GACAAATTCATTTAGCCAATTTATGGCACAAATTTGATTTGTGTCATAAGG
 AAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
 GAATTTAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCC
 TAAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
 TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAAT
 AATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4908

STRAIN M781

AAACATCCGATACCTTAATGATCA
 AAAATCCTTAGCAATTTGTTGAACAGATAGAATATGATTTGGATAAAATTCG
 ATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATTCGCGTTATG
 GATAGAGAAATCAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCT
 TTCAATTTGGTTGTGACTTTGATACAAGGTTTGAAAGAGTCGATAATGGAC
 AAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAA
 TTATTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAATCAGCCCT
 AGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCTTTTCTAA
 TCGTGTGAGAAGGTGTTTTAATGTTTCTAAAAGAGATGACGTAGAGACT
 TTTCTTCAATCCTGACAAATtCATTTAGCCAATTTATGGCACAAATTTGA
 TTTGTGTCATAAGGAAATGATTAATAAAGGAAAGCAACATGATACAGTAA
 AGTATATGGATACAGAATTTAGTTTGGTATCACAGATGGTCATGAGATT
 GTGGATTTAgACCCTAATTAAGCAAATAAATCTGATTAACTTTACAGA
 TGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAA
 TTCGTAAATTTAATAATtGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4909

STRAIN CJB110

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA
 TTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTCAGAAGCT
 TCTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
 AAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTG
 GACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTAT
 AACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGA
 GCATGAAAGAGTTACTAATATAGCAAATCAGCCATAGATGAAACTTGA
 CACGGGAGGTAAATCCCCAAAATGCCCTTTTCTAATCGTGTGAGAAGGT
 GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCAATCCT
 GACAAATTCATTTAGCCAATTTATGGCACAAATTTGATTTGTGTCATAAGG
 AAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
 GAATTTAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCC
 TAAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
 TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAAT
 AATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4910

STRAIN 1169NT

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAAT
 TGTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTCAGAAGCTT

Table 49: Comparative Sequences related to SAG1502

CTTTTATGCAACATTAGCTAGAATTTCGCGTTATGGATAGAGAAATCAAA AAATTTATTAGAGAAAATCCAAATAGTCATATCCTTTCTATTGGTTGTGG ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTGAAGAG CATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGAC ACAGGAGGTAAATCCCCAAATGCCCTTTTCTGATCGTGTGAGAAGGTG TTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCCTG ACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTGAGAAGGA AATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG AATTTTCAGTTTGGTATCAGATGGTTCATGAAATTTGTGGATTTAGACCT AAATTAAAGCAAATAAATCTGATTAACCTTTACAGATGAGATGAGCAAATT TGAGTTAGGCACACTTCGCTCTTACTTCCAACAATTCGTAAATTTAATA ATTGTTTAGGTGTGTACGAATATAAAGCATC				
SEQ ID NO: 4911 STRAIN JM9130013 AGCAATTGTTGAACAGATAGAATATGATT TTGATAAAATTCGATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGA ATTTCGCGTTATGGATAGAGAAAATCAAAAAATTTATTAGAGAAAATCCAAA TAGTCATATCCTTTCAATTGGCTGTGGACTTGATACAAGGTTTGAAAGAG TCGATAATGGACAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATG GAGATAAGAAAATTATTTTTTGAAGAGCATGAAAGAGTTACTAATATAGC AAAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAAATCCCCAAATG CCCCTTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGAT GACGTAGAGACTTTTCTTCATATCCTGACAAATTCATTTAGCCAATTTAT GGCACAATTTGATTTGTGTGAGAAGGAAATGATTAATAAAGGAAAGCAAC ATGATACAGTAAAGTATATGGATACAGAATTTAGTTTGGTATCAGAT GGTCATGAAATTTGTGGATTTAGACCTTAAATTAAAGCAAATAAATCTGAT TAACCTTACAGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTT TACTTCCAACAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATAT AAAGCATC				
PRETTY of: /biotmp/msa42193.2{*} January 21, 2003 05:04 ..				
msa42193.2{176_090}	1	50		
msa42193.2{176_CJB110}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_18RS21}	-AACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_2603}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_A909}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_COH1}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_M732}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_M781}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_H36B}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
msa42193.2{176_JM9130013}	-----	---AGCAATTG TTGAACAGAT		
msa42193.2{176_1169NT}	AAACATCCGA TACTtaatga tcaaaaatcc	ttAGCAATTG TTGAACAGAT		
Consensus	*****	*****		
msa42193.2{176_090}	51	100		
msa42193.2{176_CJB110}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_18RS21}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_2603}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_A909}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_COH1}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_M732}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_M781}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_H36B}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_JM9130013}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
msa42193.2{176_1169NT}	AGAATATGAT TTtGATAAAT TCGATAATTC	AGAAGCTTCT TTTTATGCAA		
Consensus	*****	*****		
msa42193.2{176_090}	101	150		
msa42193.2{176_CJB110}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_18RS21}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_2603}	CATTAGCTAG AwTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_A909}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_COH1}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_M732}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_M781}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_H36B}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_JM9130013}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
msa42193.2{176_1169NT}	CATTAGCTAG AaTTCGCGTT ATGGATAGAG	AAATCAAAAA ATTTATTAGA		
Consensus	*****	*****		
msa42193.2{176_090}	151	200		
msa42193.2{176_CJB110}	GAAAATCCAA ATAGTCAaAT CCTTTCaATT	GGtTGTGGAC TTGATACAAG		
msa42193.2{176_18RS21}	GAAAATCCAA ATAGTCAaAT CCTTTCaATT	GGtTGTGGAC TTGATACAAG		
msa42193.2{176_2603}	GAAAATCCAA ATAGTCAaAT CCTTTCaATT	GGtTGTGGAC TTGATACAAG		
msa42193.2{176_A909}	GAAAATCCAA ATAGTCAaAT CCTTTCaATT	GGtTGTGGAC TTGATACAAG		
msa42193.2{176_COH1}	GAAAATCCAA ATAGTCAaAT CCTTTCaATT	GGtTGTGGAC TTGATACAAG		

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_M732}	GAAAATCCAA	ATAGTCAaAT	CCTTTTCaATT	GGtTGTGGAC	TTGATACAAG		
msa42193.2{176_M781}	GAAAATCCAA	ATAGTCAaAT	CCTTTTCaATT	GGtTGTGGAC	TTGATACAAG		
msa42193.2{176_H36B}	GAAAATCCAA	ATAGTCAaAT	CCTTTTCaATT	GGcTGTGGAC	TTGATACAAG		
msa42193.2{176_JM9130013}	GAAAATCCAA	ATAGTCAaAT	CCTTTTCaATT	GGcTGTGGAC	TTGATACAAG		
msa42193.2{176_1169NT}	GAAAATCCAA	ATAGTCAaAT	CCTTTTCaATT	GGtTGTGGAC	TTGATACAAG		
Consensus	*****	*****-*	*****-***	**-*****	*****		
msa42193.2{176_090}	201	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	250
msa42193.2{176_CJB110}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_18RS21}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_2603}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_A909}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_COH1}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_M732}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_M781}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_H36B}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_JM9130013}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
msa42193.2{176_1169NT}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG	CTTGATTTCG	
Consensus	*****	*****	*****	*****	*****	*****	
msa42193.2{176_090}	251	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	300
msa42193.2{176_CJB110}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_18RS21}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_2603}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_A909}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_COH1}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_M732}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_M781}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_H36B}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_JM9130013}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
msa42193.2{176_1169NT}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT	TGAAAGAGTT	
Consensus	*****	*****	*****	*****	*****	*****	
msa42193.2{176_090}	301	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA	350
msa42193.2{176_CJB110}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_18RS21}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_2603}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_A909}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_COH1}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_M732}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_M781}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_H36B}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_JM9130013}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
msa42193.2{176_1169NT}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA	gGGAGGTAAA	
Consensus	*****	*****	*-*****	*****	*****	-*****	
msa42193.2{176_090}	351	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	400
msa42193.2{176_CJB110}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_18RS21}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_2603}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_A909}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_COH1}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_M732}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_M781}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_H36B}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_JM9130013}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
msa42193.2{176_1169NT}	TCCCCAAAAT	GCCCCTTTTC	TgATCGTGTC	AGAAGGTGTT	TTAATGTTTC	TTAATGTTTC	
Consensus	*****	*****	*-*****	*****	*****	*****	
msa42193.2{176_090}	401	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	450
msa42193.2{176_CJB110}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_18RS21}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_2603}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_A909}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_COH1}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_M732}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_M781}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_H36B}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_JM9130013}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
msa42193.2{176_1169NT}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT	AAATTCATTT	
Consensus	*****	*****	*****	*****	*****	*****	
msa42193.2{176_090}	451	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CAcAAGGAAA	TGATTAATAA	500
msa42193.2{176_CJB110}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CAcAAGGAAA	TGATTAATAA	TGATTAATAA	
msa42193.2{176_18RS21}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CAcAAGGAAA	TGATTAATAA	TGATTAATAA	
msa42193.2{176_2603}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CAcAAGGAAA	TGATTAATAA	TGATTAATAA	
msa42193.2{176_A909}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CAcAAGGAAA	TGATTAATAA	TGATTAATAA	

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_COH1}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAtAAGGAAA	TGATTAATAA
msa42193.2{176_M732}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAtAAGGAAA	TGATTAATAA
msa42193.2{176_M781}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAtAAGGAAA	TGATTAATAA
msa42193.2{176_H36B}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
msa42193.2{176_JM9130013}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
msa42193.2{176_1169NT}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
Consensus	*****	*****	*****	***-*****	*****
msa42193.2{176_090}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_CJB110}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_18RS21}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_2603}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_A909}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_COH1}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M732}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M781}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_H36B}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_JM9130013}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_1169NT}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
Consensus	*****	*****	*****	*****	*****-*
msa42193.2{176_090}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_CJB110}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_18RS21}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_2603}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_A909}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_COH1}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_M732}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_M781}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_H36B}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_JM9130013}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_1169NT}	GTATCACAGA	TGGTCATGAg	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_CJB110}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_18RS21}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_2603}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_A909}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_COH1}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M732}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M781}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_H36B}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_JM9130013}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_1169NT}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_CJB110}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_18RS21}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_2603}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_A909}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_COH1}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_M732}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_M781}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_H36B}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_JM9130013}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_1169NT}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTTAATAAT	TGTTTAGGTG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_CJB110}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_18RS21}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_2603}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_A909}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_COH1}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M732}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M781}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_H36B}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_JM9130013}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_1169NT}	TGTACGAATA	TAAAGCATC			
Consensus	*****	*****			

SEQ ID NO: 4912

STRAIN 2603 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARXRVMDREIKKFIRENPNSQILSI
 GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
 APFLIVSEGVLMLKEDDVETFLHILTNFSFSQFMAQFDLCHKEMINKGKQHDVTVKYMDTE

Table 49: Comparative Sequences related to SAG1502

FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4913

STRAIN 090 frame: 2

NDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLD
TRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVNPNQAPFLI
VSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTEFQFGI
TDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4914

STRAIN A909 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4915

STRAIN H36B frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4916

STRAIN 18RS21 frame: 3

HPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIG
CGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
PFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4917

STRAIN M732 frame: 1

KHPILNDQKSLAIVEQIEYDLDFKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4918

STRAIN COH1 frame: 1

KHPILNDQKSLAIVEQIEYDLDFKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4919

STRAIN M781 frame: 1

KHPILNDQKSLAIVEQIEYDLDFKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4920

STRAIN CJB110 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4921

STRAIN 1169NT frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTQEVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

SEQ ID NO: 4922

STRAIN JM9130013 frame: 2

AIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSIGCGLDTRFERV
DNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQAPFLIVSEGVL
MFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHD TVKYMDTEFQFGITDGHEI
VDLDPKPKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVY EYKA

PRETTY of: /biotmp/msa42204.2{*} January 21, 2003 05:05 ..

	1		50
msa42204.2{176_H36B}	khpilndqks	laiveqieyd fdkfdNSEAS	FYATLARiRV MDREIKKFIR
msa42204.2{176_JM9130013}	-----	-AIVEQIEYD fdkfdNSEAS	FYATLARiRV MDREIKKFIR
msa42204.2{176_090}	-----ndqks	laiveqieyd fdkfdNSEAS	FYATLARiRV MDREIKKFIR
msa42204.2{176_18RS21}	-hpilndqks	laiveqieyd fdkfdNSEAS	FYATLARiRV MDREIKKFIR
msa42204.2{176_2603}	khpilndqks	laiveqieyd fdkfdNSEAS	FYATLARxRV MDREIKKFIR
msa42204.2{176_A909}	khpilndqks	laiveqieyd fdkfdNSEAS	FYATLARiRV MDREIKKFIR
msa42204.2{176_CJB110}	khpilndqks	laiveqieyd fdkfdNSEAS	FYATLARiRV MDREIKKFIR

Table 49: Comparative Sequences related to SAG1502

msa42204.2{176_COH1}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
msa42204.2{176_M732}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
msa42204.2{176_M781}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
msa42204.2{176_1169NT}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
Consensus	-----	*****	*****	*****	*****
51					
msa42204.2{176_H36B}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_JM9130013}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_090}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_18RS21}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_2603}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_A909}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_CJB110}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_COH1}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M732}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M781}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_1169NT}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
Consensus	*****	*****	*****	*****	*****
101					
msa42204.2{176_H36B}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_JM9130013}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_090}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_18RS21}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_2603}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_A909}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_CJB110}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_COH1}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_M732}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_M781}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
msa42204.2{176_1169NT}	TNIAKSALDE	TWTrEVNPQN	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSF
Consensus	*****	***	*****	*****	*****
151					
msa42204.2{176_H36B}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_JM9130013}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_090}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_18RS21}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_2603}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_A909}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_CJB110}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_COH1}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_M732}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_M781}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_1169NT}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
Consensus	*****	*****	*****	*****	*****
201					
msa42204.2{176_H36B}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_JM9130013}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_090}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_18RS21}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_2603}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_A909}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_CJB110}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_COH1}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M732}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M781}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_1169NT}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
Consensus	*****	*****	*****	*****	
239					

Table 50: Comparative Sequences relating to SAG 1024

SEQ ID NO. 5001

STRAIN 2603

ATGAAAAAACAATACTATTACTGCTTATTGGAGGCTTATTAATAATGATAATGATGACA
 GCATGTAAGGATTCAAAAATCCAGAAAACCGCACAAAGGAAGAGTACCAAGCTGAACAA
 AATTTTAAACCGTTTGTGAGTTTGTAGCACAAAAGATAAAGATTTGAGCAAAATACAA
 AAATACTTACTATTAGTATCGGATTGAGGTGATGCATTAGATTTAGAATATTTCTATAGT
 ATTCAAGATTTAAAAAATAAGGATTTAGGGAGGTTTGAACAAGAAAAAGTCAAATA
 GAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAAGAGGTCCCATTTGAATATTTTAAA
 AATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTGATGACTTTATTATCGGA
 GCAATGGATACTAAAGAATTAAAAAGAAATTAATAAAGTAAAAAGTTATTATTATTA
 AAACATCCGGAACCTGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCGAAGCTT
 ATTAAAAAA

SEQ ID NO. 5002

STRAIN 090

TAAGGATTCAAAAATCCAGAAAACCGCACAAAG
 GAAGAGTACCAAGCTGAACAAAATTTTAACTGTTTTTGTAGTTTTTGTAGC
 ACAAAAATATAAAGATTTGAACAAAATACAAAATACTTACTATTAGTAT
 CGGATTTCAGGTGATGCATTAGATTTAGAATATTTCTATAGTATTCAAGAT
 TTAATAAATAAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAAT
 AGAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAAGAGGTCCCATTTG
 AATATTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACA
 TTTGATGACTTTTATTATCGGAGCAATGGATACTAAAGAATTAAAAAATT
 AAAAGTAAAAAGTTATTATTAAAAACATCCGGAACCTGAGTTGAAAGATA
 TAACATATGAATTGCCGACACAGTCGAAGCTTATTAAAAAA

SEQ ID NO. 5003

STRAIN 18RS21

TAAGGATTCAAAAATCCAGAAAACCGCACAAAGGAAG
 AGTACCAAGCTGAACAAAATTTTAAACCGTTTTTGTAGTTTTTGTAGCACA
 AAAGATAAAGATTTGAGCAAAATACAAAATACTTACTATTAGTATCGGA
 TTCAGGTGATGCATTAGATTTAGAATATTTCTATAGTATTCAAGATTTAA
 AAAAAATAAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAATAGAA
 AAGCCGGTGGCTATAATGAGTTAGAAAATAAAGAGGTCCCATTTGAATA
 TTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTG
 ATGACTTTTATTATCGGAGCAATGGATACTAAAGAATTAAAAAGAAATTAAAA
 GAATTAAAAAATAAAGTAAAAAGTTATTATTAAAAACATCCGGAAC
 TGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCGAAGCTTATTAA
 AAAAA

PRETTY of: /biotmp/msa212269.2(*) February 10, 2003 05:07 ..

msa212269.2{184_090}	1	50
msa212269.2{184_2603}	atgaaaaaac aaaaactatt actgcttatt ggaggcttat taataatgat	
msa212269.2{184_18RS21}	*****	
Consensus	*****	
msa212269.2{184_090}	51	100
msa212269.2{184_2603}	-----TAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG	
msa212269.2{184_18RS21}	aatgatgaca gcatgTAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG	
Consensus	*****	
msa212269.2{184_090}	101	150
msa212269.2{184_2603}	AAGAGTACCA AGCTGAACAA AATTTTAAAC tGTTTTTTGA GTTTTTTAGCA	
msa212269.2{184_18RS21}	AAGAGTACCA AGCTGAACAA AATTTTAAAC cGTTTTTTGA GTTTTTTAGCA	
Consensus	*****	
msa212269.2{184_090}	151	200
msa212269.2{184_2603}	CAAAAAtATA AAGATTTGAa CAAAATACAA AAATACTTAC TATTAGTATC	
msa212269.2{184_18RS21}	CAAAAAGATA AAGATTTGAg CAAAATACAA AAATACTTAC TATTAGTATC	
Consensus	*****	
msa212269.2{184_090}	201	250
msa212269.2{184_2603}	GGATTCAGGT GATGCATTAG ATTTAGAATA TTTCTATAGT ATTCAAGATT	
msa212269.2{184_18RS21}	GGATTCAGGT GATGCATTAG ATTTAGAATA TTTCTATAGT ATTCAAGATT	
Consensus	*****	
msa212269.2{184_090}	251	300
msa212269.2{184_2603}	TAAAAAATAA TAAGGATTTA GGAAGTTTG AAACAAGAAA AAGTCAAATA	
msa212269.2{184_18RS21}	TAAAAAATAA TAAGGATTTA GGAAGTTTG AAACAAGAAA AAGTCAAATA	
Consensus	*****	
msa212269.2{184_090}	301	350
msa212269.2{184_2603}	GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTGGA	
msa212269.2{184_18RS21}	GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTGGA	
Consensus	*****	

Table 50: Comparative Sequences relating to SAG 1024

	351		400
msa212269.2{184_090}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT		
msa212269.2{184_2603}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT		
msa212269.2{184_18RS21}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT		
Consensus	*****	*****	*****
	401		450
msa212269.2{184_090}	TTGATGACTT TATTATCGGA GCAATGGATA CT.....	
msa212269.2{184_2603}	TTGATGACTT TATTATCGGA GCAATGGATA CT.....		.aaagaatta
msa212269.2{184_18RS21}	TTGATGACTT TATTATCGGA GCAATGGATA CTaaagaatt		aaaagaatta
Consensus	*****	*****	*****
	451		500
msa212269.2{184_090}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTTATTAA AACATCCGGA		
msa212269.2{184_2603}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTTATTAA AACATCCGGA		
msa212269.2{184_18RS21}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTTATTAA AACATCCGGA		
Consensus	*****	*****	*****
	501		550
msa212269.2{184_090}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA		
msa212269.2{184_2603}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA		
msa212269.2{184_18RS21}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGgCACAG TCGAAGCTTA		
Consensus	*****	*****	*****
	551		
msa212269.2{184_090}	TTAAAAAA		
msa212269.2{184_2603}	TTAAAAAA		
msa212269.2{184_18RS21}	TTAAAAAA		
Consensus	*****		

SEQ ID NO. 5004

STRAIN 2603 frame: 1

MKKQKLLLLIGLLIMIMMTACKDSKIPENRTKEEYQAEQNFKPFEEFLAQKDKDLSKIQ
 KYLLLVSDSGDALDLEYFYISIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFK
 NNIVYPKGKPNITFDDFIIGAMDTKELKELKKLVKSYLLKHPETELKDITYELPTQSKL
 IKK

SEQ ID NO. 5005

STRAIN 090 frame: 2

KDSKIPENRTKEEYQAEQNFKLFEEFLAQKYKDLNKIQKYLVLVSDSGDALDLEYFYISIQ
 DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAM
 DTKEKELKKLVKSYLLKHPETELKDITYELPTQSKLIKK

SEQ ID NO. 5006

STRAIN 18RS21 frame: 2

KDSKIPENRTKEEYQAEQNFKPFEEFLAQKDKDLSKIQKYLVLVSDSGDALDLEYFYISIQ
 DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAM
 DTKEKELKELKKLVKSYLLKHPETELKDITYELPAQSKLIKK

PRETTY of: /biotmp/msa212547.2{*} February 10, 2003 05:11 ..

	1		50
msa212547.2{184_18RS21}	-----	--KDSKIPEN RTKEEYQAEQ NFKpFFEFLA	
msa212547.2{184_2603}	mkkqkl1111i ggllimimmt	ackDSKIPEN RTKEEYQAEQ NFKpFFEFLA	
msa212547.2{184_090}	-----	--KDSKIPEN RTKEEYQAEQ NFKlFFEFLA	
Consensus	*****	*****	***-*****
	51		100
msa212547.2{184_18RS21}	QKdKDLsKIQ KYLLLVSDSG DALDLEYFYIS IQDLKKNKDL GKFETRKSQI		
msa212547.2{184_2603}	QKdKDLsKIQ KYLLLVSDSG DALDLEYFYIS IQDLKKNKDL GKFETRKSQI		
msa212547.2{184_090}	QKyKDLnKIQ KYLLLVSDSG DALDLEYFYIS IQDLKKNKDL GKFETRKSQI		
Consensus	***-***-***	*****	*****
	101		150
msa212547.2{184_18RS21}	EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDTkelkel		
msa212547.2{184_2603}	EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDT...kel		
msa212547.2{184_090}	EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDT.....		
Consensus	*****	*****	*****
	151		186
msa212547.2{184_18RS21}	KELKKLVKS YLLKHPETEL KDITYELPaQ SKLIKK		
msa212547.2{184_2603}	KELKKLVKS YLLKHPETEL KDITYELPtQ SKLIKK		
msa212547.2{184_090}	KELKKLVKS YLLKHPETEL KDITYELPtQ SKLIKK		
Consensus	*****	*****	*****

Table 51: Comparative Sequences relating to SAG0677

SEQ ID NO. 5101

STRAIN 2603

ttgaataataaagggtgtcggtggcgatgggtgtccaaatattatcaatacta
 tatcaaaatggacaacaataaaaccttacttaagtcccaaagataagacta
 ctgtagagaagttagaagatcgctggaaaaaattactttcaaagttcag
 gatactggcattgggtttgaaagacgtttatcttcaatctgttaagtatgt
 tgggtgggtggcaataataatttagacctatcacacctccaggatttaaaa
 aagaagataaaaaagttgaaaaaccaaatttagaccgtccaccaggaatt
 gatttaccagcaccaacttcaatgagaagtttggattattcaaccccacc
 gggaactaagccaagcaaacccaaagatagtttatcaactcctccagggt
 tcccagatttaaacacgcgcggatgaagcaccaaaggatagtaaaaaa
 gacgctattgaagataaatcaggagcaattaaatatgctaagttcttca
 acttagctttgttgatggccctatttttagctagcaaaagtaaatggcaaaa
 tattacaagtcgaatctgatggcaaattagtcatcctagaaatgctttg
 tcagctaatacaatttgatgacactagtcttaaaatttatcgtaataataa
 tcgcaataaagaattactatcacacagattattttgcagatacaaaat
 atgtcaatatcacagcgggtgactatttgagcaatactacttttgagcaa
 ttagctactgggtgaaacagtagattaccatgccatttgtattttcaagctt
 tgctgctattaaagacaagggtggtaagatttatgttaacgataaattgc
 aagaaacttctcgtatagcgttaaagataaatctgttaagattggatt
 gaattaccaaatgatgtcagacataattgatagtttatctgttcgtcgttt
 gaatgaggttaaaactgttgataaatatcttgaaaaatgatgaacaagaca
 ttaatctcagcaaaaacttaccaattaaaatacaacccgacaaatcgtcgt
 cttagagtttactattaataacattaactcaagttcagaaatcatgaccac
 tttcaaagatggaaagatgccagaattgggttgaaacaaaagatgtttctt
 tggatataaacgatatggacatgagtaagtttaaaactatcgcacttggga
 cgaaaggattctgaatttaagggaacacttattgcaaaaactggaacagt
 tgaattagatatgtttttcaaacaatctcaagaccagcttcaattatta
 aaaaaatataccttatccaaaatgggtgttccaaatgaattgaaaaaattt
 gactctagttttgggttaactgaaagttagatagatggatactatattta
 taaagatgcaattaaaccttaaatttaaattaaccagtggtgcaagctta
 aagttgtttataaagggaagatccatatagtcacagaaagaagat
 atgactaaaaaagggtgaacagctcagtcattcaactcaagccaatgaaaa
 tacagcaaaagtaacctttgctaataattgactgggtcacattatagtaagg
 ttactgtgaatgggaaagaagttgttaaaggtagtgagttacctttaact
 aaaggatggacaacatttgtattacataaaacagaaaaattcattaaatgt
 taaaagtttgattatggagacgggttagtgtaagtaagaaagttcaacaac
 ttcttttaagttcctagattatctaaaaataagcatatgagggatagcta
 ctactatgcaaaaagattcagcgtattacgaaacaagtgacagtttagt
 ccttcgaattaatctcactgcagatactaaacttaattttaatgctgtta
 aaggagcagtgctcttactgaaaatatgatgatgagacagtttgagtt
 gctggaccacaagatgatcctgttagtgacataaatacccatcagttat
 tctcttaactcctgccttatggaaactgctagtgaggcaactctaaatg
 gtaaggaaatcacagcatctggatttatcggtcacatcaaggatgggtgat
 aaaagcaagcatgttgaaagtaaaatgggtgaatgaaaatggagacatgct
 aggaacccctgttattattcaaggtaagacttgactaatcgaacaaaac
 cattaatgagtgagcgttagagtttatgcccgttaacaatatgagttc
 cgggtcaaataccacttagtcgttttaacacttggattagggttgaagt
 ggtaacagaagcaggagagaaagcaagattgttcgtcgcattgttcttg
 accaatcagttccagagcttaacacagcagttgctaaacgtgatttgact
 tctgatactgctcttatccacatcggttgccaaagatgactctctaaaact
 aaaattatatcaagatgattcattacttgaatctgttgataaaacgggtc
 tttatagttttagaatgggttagaaatcactaaagatatgacagttacca
 ctagaatttggagataaatattttaagttatctgctgttgacttatcaaa
 ttatcgtcgtaatgagacccttcatatctatagaaacggttttgatgtta
 aagcaagccaaatgacagctgacaaaggagctaaagtaactgtggatag
 ttgatgaagcacttagttgttccagaaatggcaggagcttatacattaac
 aatcgacgaagctccaaacacaaatgaatcaggaatgttaacaaacgcta
 aagtatcgattcattatgttaaatgggtgggtgttgataaagttgatgttccg
 attaaagtagttgacttagaagctattcgtaaagctgaagaagcacgtaa
 agctgaagaagcacgtaagctgaagaagcacgtaagctgaagaagggac
 ataaaacccaagaagcacctatagttgaagaaggctacaagggttaataac
 gttcatcaaactgatactacagttaaagcgtctgatttaccaaagactaa
 gacagtttccgcagttcatatggctagaacagacaataaaacagataactt
 cacatcagacacatgttgaaaaacaaattaaaaatacattgccatccact
 ggtgacagcaaacgtgggttatttatcactgggaatggctatcgttatgct
 gagtgtattatttagtttagctaaaaagtttaaaagcaaatat

SEQ ID NO. 5102

STRAIN A909

TTGAATAATAAAGGTGTGCGTGGCGAT

GGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTA
 CTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGA
 AAAAAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTT
 TATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCT
 TATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAA
 AATTAGACCGTCCACCAGGAATTGATTTACCACCACCACTTCAATGAGA
 AGTTTTGATTATTCAACCCACCGGGAACCTAAGCCAAGCAACCCCAAAGA
 TAGTTTATCAACTCCTCCAGGTTTCCAGATTAAACACGCCGCCCGGATG
 AAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCA
 ATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTT
 AGCTAGCAAAGTAAATGGCAAATATTACAAGTCGAATCTGATGGCAAAT
 TAGTCATTCTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAGT

Table 51: Comparative Sequences relating to SAG0677

CTTAAAAATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAAAC
 AGATTATTTTGAGATACAAAATATGTCAATATCACAGCGGTTGACTATT
 TGAGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTAC
 CATGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAA
 GATTTATGTTAAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAG
 ATAAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATT
 GATAGTTTATCTGTTCTGCTGTTGAATGAGGTTAAAACTGTTGATAATAT
 CTTGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAA
 AATACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAAAC
 TCAAGTTTCAGAAATCATGACCCTTTCAAAGATGGAAAGATGCCAGAATT
 GGTGAAaCAAAAAGATGTTCTTTGGATATAaaCGATATGGACATGAGTA
 AGTTTAAAACTATTGACTTTGGACGAAAGGATTCTGAATTAAAGGGACAA
 CTTATTGCAAAAAGCTGGAACAGTTGAATTAGATATGTTTTTCAAACAATC
 TCAAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAATGGTG
 TTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGT
 CAGATAGATGGATACTATATTATAAAGATGCAATTAACCTTAAATTTAA
 ATTAACCAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATC
 CATATAGTCAATCAGAAAGAGATATGACTAAAAAAGGTGAACAGCTCAGT
 CATTCAACTCAAGCCAATGAAAAATACAGCAAAAGTAACCTTTGCTAATAT
 TGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGTA
 AAGGTAGTGAAGTTACCTTTAACTAAAGGATGGACAACATTGTATTACAT
 AAAACAGAAAAATTCATTAAATGTTAAAAAGTTTGATTATGGAGACGGGTAG
 TGTAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTTAGATTATCTAAAA
 ATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTAGCGTAT
 TACGAaaCAAGTGACAGTCTAGTCTTGAATTAATCTCACTGCAGATAC
 TAAACTTTAATTTTAAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATA
 TGATGATGAGACAGTTTGCAAGTTGCTGGACCACAAGATGATCTGTAGT
 GAACATAAATACCCATCAGTATTTCTCTTAACTCTGCTTATTGGAAAC
 TGCTAGTGAGGCAACTCTaAATGGTAAGGAAATCACAGCATCTGGTATTA
 TCGGTCAATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATG
 GTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAA
 AGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTT
 ATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCTGTTT
 AACACTTGGATTAGGGTTGAAGTGGTAACAGAGCAGGAGAGAAAGCAAG
 TATTGTTCTGTCGATGTTCTTTGACCAATCAGTCCAGAGCTTAACACAG
 CAGTTGCTAAACGTGATTTGACTTTCTGATCTGCTCTTATCCACATCGTT
 GCCAAAGATGACTCTCTAAACTAAATTTATATCAAGATGATTCACTACT
 TGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAA
 TCACTAAAGATATGACAGTACCACTAGAATTTGAGATAATATTATTAAAG
 TTATCTGCTGTTGACTTATCAAATATCTGTCGTAATGAGACCCCTTCATAT
 CTATAGAAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAG
 GAGCTAAAGTAACGTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAA
 ATGGCAGGAGCTTATACATTAAACAATCGACGAAGATCCAAACACAAATGA
 ATCAGGAATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAATGGTG
 GTGTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATT
 CGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGA
 AGCAGCTAAAGCTGAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTG
 AAGAGGGACATaAAACCCAAAGACCTTATAGTTGAAGAAGGCTACAAG
 GTTAATAACGTTTCACTCAAACTGATACTACAGTTAAAGCGTCTGATTTACC
 AAAGACTAAGACAGTTTCCGCACTTATATGGCTAGAACAGACAATAAAC
 AGATAACTTCACATCAGACACATGTTGAAAAACAAATTAAAAATA

SEQ ID NO. 5103

STRAIN H36B

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTT
 ACCTAAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGaaGATCGCTGG
 AAAAAAATTACTTTCAAAGTTCAAGGATCTGGCATTGGTTTGAAAGACGT
 TTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAAATTTAGACC
 TTATCACACCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAACCA
 AAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAG
 AAGTTTTGATTATTCAACCCACCGGGAACCTAAGCCAAGCAAAACCAAAG
 ATAGTTTATCAACTCTCCAGGTTTCCAGATTTTAAACACGCCCGCGGAT
 GAAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGC
 AATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCCTATTT
 TAGCTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAA
 TTAGTCATTCTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAG
 TCTTAAATTTATCGTAATAATAATCGCAATAAAGAAATTaCTATCAAA
 CAGATTATTTTGAGATACAAAATATGTCAATATCACAGCGGTTGACTAT
 TTGAGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAaCAGTAGATT
 CCATGCCATTGTATTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTA
 AGATTTATGTCAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAA
 GATAAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATAT
 TGATAGTTTATCTGTTCTGCTGTTGAATGAGGTTAAAACTGTTGATAATA
 TCTTGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTA
 AAATACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATAACATTAA
 CTCAAGTTCAAGAAATCATGACCCTTTCAAAGATGGAAAGATGCCAGaAT
 TGTTTGAACAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGT
 AAGTTTAAACTATTGACTTTGGACGAAAGGATTCTGAATTTAAGGGACA
 ACTTATTGCAAAAAGCTGGAACAGTTGAATTAGATATGTTTTTCAAACAAT
 CTCAAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAATGGT
 GTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAG
 TCAGATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAATTTA
 AATTAACCAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGAT

Table 51: Comparative Sequences relating to SAG0677

CCATATAGtCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAG
 TCATTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATA
 TTGACTGGTCACATTATAGTAAGGTACTGTGAATGGAAAAGAAGTTGGT
 AAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACA
 TAAAAACAGAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGT
 GTGTAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTTAGATTATCTAAA
 AATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTA
 TTACGAAACAAGTGACAGTCTAGTCTTCTGAATTAATCTCACTGCAGATA
 CTAAACTTAATTTTAAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAAT
 ATGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAG
 TGAACATAAATAACCATCAGTATTTCTCTTAACCTCCTGCCTTATTGGAAA
 CTGCTAGTGAGGCaACTCTAAATGGTAAGGAAATCACAGCATCTGGTATT
 ATCGGTTCACATCAAGGATGGtGATAAAAGCAAGCATGTTGAAGTCAAAAT
 GGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTA
 AAGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTT
 TATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCCTTAGTCGTTT
 TAACaCTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAAGCAA
 GTATTGTTCTGTCGATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACA
 GCAGTTGCTAAACGTGATTGACTTCTGATACTGCTCTTATCCACATCGT
 TGCCAAAGATGACTCTCTAAACTTAAATTTATATCAAGATGATTATTAC
 TTGAATCTGTGATAAAACCGGTCTTTATAGTTTGTAGAAATGGTGTAGAA
 ATCACTAAAAGATATGACAGTACCCTAGAATTTGGAGATAATATTACTAA
 GTTATCTGCTGTTGACTTATCAAATTATCGTCTGAATGAGACCCTTCATA
 TCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAA
 CGAGCTAAAGTAAGTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGA
 AATGGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATG
 AATCAGGAATGTTAAACAAACGCTAAAGTATCGATTCAATTATGTAATGGT
 GGTGTTGATAAAGtGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTAT
 TCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAG
 AAGCACGTAAAGCTGACGAAGCACATAAAGCTGAAGAAGTACGTAAAGCT
 GAAGAAGCACATAAAGTGAAGAAGCACGTAAAGCTGAAGAAGGACATAA
 AACCCAAAGAAGCACCTATAGTTGAAGAAGGCTACAAGGTTAATAACGTTT
 ATCAAACGTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACA
 GTTTCGCGAGTTTATATGGCTAGAACAGACAATAAACAGATAACTTCACA
 TCAGACACATG

SEQ ID NO. 5104

STRAIN 18RS21

TTGAATAATAAAGGTGTCTGGTGGCGATGGTGTCCAA
 ATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAAGTCC
 CAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAATTA
 CTTTCAAAGTTTCAAGGATACTGGCATTTGGTTTGAAAGACGTTTATCTTCAA
 TCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACACC
 TCCAGGATTTAAAAAGAAGATAAAAAAGTTGAAAAACCAAATTAGACC
 GTCCACCAGGAATTGATTTACCAGCACCACTTCAATGAGAAGTTTGTAT
 TATTCAACCCACCGGGAACCTAAGCCAAAGCAAACCCAAAGATAGTTTATC
 AACTCCTCCAGGTTTCCAGATTTAAACACGCCCGCGGATGAAGCACCAA
 AGGATAGTAATAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAATAT
 GCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCCTATTTTAGCTAGCAA
 AGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAATTAGTCATTC
 CTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAGTCTTAAAAAT
 TATCGTAATAATAATCGCAATAAAGAAATTAATATCACAAACAGATTATTT
 TGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTGAGCAATA
 CTACTTTTGAAGCAATTAGCTACTGGTGAACAGTAGATTACCATGCCATT
 GTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTATGT
 TAACGATAAATTGCAAGAAaACTTCTCGTATAGCGCTTAAAGATAAATCTG
 TTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATTGATAGTTTA
 TCTGTTCTGTCGTTTGAATGAGGTTAAACTGTTGATAATATCTTGAAAAA
 TGATGAACAAGACATTAATCTCAGCAAaACTTACCAATTAAAAATACAACC
 CGACAAATCGTCGTCTAGAGTTTACTATTAAATAACATTAACCTCAAGTTCA
 GAAATCATGACCCTTTCAAAGATGGAAAGATGCCAGAATTGGTTGAACA
 AAAAGATGTTTCTTTGGATATaAACGATATGGACATGAGTAAGTTTAAAA
 CTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGGACAACCTTATTGCA
 AAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTCAAGACCC
 AGCTTCAATTATTAAAAAATATACCTTATCCAAATGGTGTTCCAAATG
 AATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATAGAT
 GGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAATTAACCAG
 TGGTGAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATAGTC
 ATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCAACT
 CAAGCCAATGAAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTGGTC
 ACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGTTAAAGGTAGTG
 AGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACAGAA
 AATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGTAGTGAAGTAA
 GAAAGTTCAACAACCTTCTTTAAGTCTTAGATTATCTAAAAATAAGCATA
 TGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTACGAAACA
 AGTGACAGTCTAGTCTTCTGAATTAATCTCACTGCAGATACTAACTTAA
 TTTTAAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATGATGATGA
 GACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGAACATAAA
 TACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGGAACTGCTAGTGA
 GGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTCACT
 TCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGTGAATGAA
 AATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAGACTTGAC
 TAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCGGTA

Table 51: Comparative Sequences relating to SAG0677

AACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTTAACACTTGG
 ATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGTTCCG
 TCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAACACAGCAGTTGCTA
 AACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAAGAT
 GACTCTCTAAAACTAAAATTATATCAAGATGATTCACTTACTTGAATCTGT
 TGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAATCACTAAAG
 ATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAGTTATCTGCT
 GTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATATCTATAGAAA
 CCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTAAAG
 TAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCAGGA
 GCTTATACATTAAACAATCGACGAAGCTCCAAACACAAATGAATCAGGAAT
 GTTAACAAACGCTAAAGTATCGATTCAATTATGTAAATGGTGGTGTGATA
 AAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAAAGCT
 GAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTGAAGAGGGACATAA
 AACCCAAAGAAGCACCTATAGTTGAAGAAGGCTACAAGGTTAATAACGTTT
 ATCAAACGTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACA
 GTTTCGCGAGTTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACA
 TCAGACACATGTTGAA

SEQ ID NO. 5105

STRAIN M732

TTGAATAATAAAGGTGTCGGTGGCGATGGTGTCC

AAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGT
 CCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAT
 TACTTTCAAAGTTCAGGATACTGGCATTGGTTTTGAAAGACGTTTATCTTC
 AATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACA
 CCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAACCAAAATTAGA
 CCGTCCacCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGTTTTG
 ATTATTC AACCCACCGGGAATAAGCCAAGCAAACCCAAAGATAGTTTA
 TCAACTCCTCCAGTTTCCAGATTTAAACACGCCCGCGGATGAAGCCAC
 CAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAA
 TATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTTAGCTAG
 CAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCA
 TTCTTAGAAATGCTTTGTGCTAGCTAATCAATTTGATGACACTAGTCTTAAA
 ATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAGATTA
 TTTTGCAGATACAAAATATGTCATATCACAGCGGTTGACTATTTGAGCA
 ATACTACTTTTGGAGCAATTAGCTACTGGTGAACAGTAGATTACCATGCC
 ATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTA
 TGTTAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAGATAAAT
 CTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATTGATAGT
 TTATCTGTTCTGCTGTTTGAATGAGGTTAAAACTGTTGATAATATCTTGAA
 AAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTAAAATACA
 ACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATAACATTAACCTCAAGT
 TCAGAAATCATGACCCTTTCAAAGATGGAAAGATGCCAGAATTGGTTGA
 ACAAAAAGATGTTTTCTTTGGATATAAACGATATGGACATGAGTAAGTTTA
 AAATATTCTGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACCTATT
 GCAAAAACCTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTCAAGA
 CCCAGCTTCAATTATTAAAAAATATACCTTATCCAAAATGGTGTTCCAA
 ATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATA
 GATGGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAATTAAC
 CAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATA
 GTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCA
 ACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTG
 GTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGTAAAGGTA
 GTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACA
 GAAAATTCAATAATGTTAAAGTTTGATTATGAGACCGGTAGTGTAAAG
 TAAGAAAGTTCAACAACITCTTTAAGTCTTAGATTATCTAAAAATAAGC
 ATATGAGGGATATGCTACTTACTATGCAAAAAGATTACGCGTATTACGAA
 ACAAGTGACAGTCTAGTCCCTCGAATTAATCTCACTGCAGATACTAAACT
 TAATTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATGATGA
 TGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTaGTGAACAT
 AAATACCCATCAGTaTTCTCTTAACTCCTGCCTTATTGGAAaCTGCTAG
 TGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTC
 ACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGTGAAT
 GAAAATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTAAAGACTT
 GACTAATCGAACAACCAATTAATGAGTGGACGTAGAGTACTTTATGCCG
 GTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCTGTTTTAACACT
 TGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGT
 TCGTTCGCTGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCAGTTG
 CTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAA
 GATGACTCTCTAAACTAAAATTATATCAAGATGATTCACTACTTGAATC
 TGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAATCACTA
 AAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAAGTTATCT
 GCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATATCTATAG
 AAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTA
 AAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCA
 GGAGCTTATACATTAAACAATCGACGAAGCTCCAAACACAAATGAATCAGG
 AATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAAATGGTGGTGTG
 ATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAAA
 GCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGAAGCACG
 TAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAAGAAG
 CACATAAAGTGAAGAAGCACGTAAAGCTGAAGAGGGACATAAAACCCAA
 GAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTCATCAAC

Table 51: Comparative Sequences relating to SAG0677

TGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGTTTCCG
CAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCAGACA
CATGTTGAAAA

SEQ ID NO. 5106

STRAIN COH1

TTGAATAATAAAGGTGTCCGGTGGCGATGGT
GTCCAAATTTATCAATACTATATCAAAATGGAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTTGAAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTAGACCTTAT
CACACCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTATTCAACCCACCGGGAACCTAAGCCAAGCAAACCCAAAGATAG
TTTATCAACTCCTCCAGGTTCCAGATTTAAACACGCCGCCGGATGAAG
CCaCCAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTTATTTTAG
CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTA
GTCAATCCTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAGTCT
TAAAAATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAAACAG
ATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTG
AGCAATACTACTTTTGGCAATTAGCTACTGGTGAACAGTAGATTACCA
TGCCATTTGTATTTTCAAGCTTTGCTGCTATTTAAAGACAAGGGTGGTAAGA
TTTATGTTAACGATAAAATGCAAGAACTTCTCGTATAGCGCTTAAAGAT
AAATCTGTTAAGATTGGTATTTGAATTACCAAAATGATGTGAGACATATTGA
TAGTTTATCTGTTCCGTCGTTTGAATGAGGTTAAAACTGTTGATAATATCT
TGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAAAA
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATAACATTAACCTC
AAGTTCAAGAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAATTGG
TTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAG
TTTAAACTATTCCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACT
TATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTC
AAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGTGT
CCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTTAACTGAAAGTCA
GATAGATGGATACTATATTATAAAGATGCAATTAACCTTAAATTTAAAT
TAACCAAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAAATGAAATACAGCAAAAGTAACCTTTGCTAATATTG
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAAGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA
AACAGAAAAATTCATTAAATGTTAAAAAGTTTGATTATGGAGACGGGTAGTG
TAAGTAAGAAAGTTCAACAACTTCTTTAAGTCTTAAGATTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA
CGAAACCAAGTGACAGTCTAGTCTTCCGAATTAATCTCACTGCAGATACTA
AACTTAATTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAATATG
ATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGA
ACATAAATACCCATCAGTATTTCTCTTAACTCCTGCTTATTGGAACTG
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC
GGTCACATCAAGGATGGTGATAAAAAGCAAGCATGTTGAAGTCAAAATGGT
GAATGAAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
ACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTTAA
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA
TTGTTCTGTCGCAATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCA
GTTGCTAAACGTGATTtGACTTCTGATACTGCTCTTATCCACATCGTTGC
CAAAGATGACTCTCTAAaCTAAATTTATATCAAGATGATTCACTTACTTG
AATCTGTTGATAAAAACCGTCTTTATAGTTTATAGAAATGGTGTAGAAATC
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTATTAAGTT
ATCTGCTGTTGACTTATCAAAATATCGTCTAATGAGACCTTCATATCT
ATAGAAAACCGTTTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA
GCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAAT
CAGGAATGTTAAACAAACGCTAAAGTATCGATTCAATTATGTAAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGAAG
CACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA
GAAGCACATAAAGTCGAAGAAGCACGTAAAGCTGAAGAGGGACATAAAAC
CCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTCATC
AACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGTT
TCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCA
GACACATGT

SEQ ID NO. 5107

STRAIN M781

TTGAATAATAAAGGTGTCCGGTGGCGATGGT
GTCCAAATTTATCAATACTATATCAAAATGGAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTTGAAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTAGACCTTAT
CACACCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTATTCAACCCACCGGGAACCTAAGCCAAGCAAACCCAAAGATAG
TTTATCAACTCCTCCAGGTTTCCAGATTTAAACACGCCGCCGGATGAAG

Table 51: Comparative Sequences relating to SAG0677

CCaCCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTATTTTAG
CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTA
GTCATTCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCT
TAAaATTTATCGTAATAATAATCGCAATAAAGAAATTaCTATCACAACAG
ATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTG
AGCAATACTACTTTTGGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA
TGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA
TTTATGTTAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAGAT
AAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGA
TAGTTTATCTGTTCTGCTGTTTGAATGAGGTTAAACTGTTGATAATATCT
TGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAAAA
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTC
AAGTTTCAAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAGAATTGG
TTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAG
TTTAAAACTATTTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAAC
TATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTC
AAGACCCAGCTTCAATTATTAAAAAATATACCTTATCCAAAATGGTGT
CCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTTAACTGAAAGTCA
GATAGATGGATACTATATTTATAAAGATGCAATTAACTTAAATTTAAAT
TAACCAAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCATCAGAAAGAAGATATGACTAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAATGAAAAATACAGCAAAAGTAACCTTTGCTAATATTG
ACTGGTCACATTATAGTAAGGTACTGTGAATGGAAAAGAAGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA
AACAGAAAATTCATTAAATGTTAAAGTTTGAATATGGAGACGGGTAGTG
TAAGTAAGAAAAGTTCAACAACCTTCTTTAAGTCTAGATTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA
CGAAACAAGTGACAGTCTAGTCTTGAATTAATCTCACTGCAGATACTA
AACTTAATTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATG
ATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGA
ACATAAATACCCATCAGTATTTCTTTAACTCCTGCTTATTGGAACTG
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC
GGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGT
GAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
ACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTTAA
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCA
GTTGCTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGC
CAAAGATGACTCTCTAAACTAAATTTATATCAAGATGATTCAATTACTTG
AATCTGTTGATAAAACCGGTCTTATAGTTTATAGAAATGGTGAGAAATC
ACTAAAGATATGACAGTACCACTAGAAATTTGGAGATAATATTATTAAGTT
ATCTGCTGTTGACTTATCAAATATCGTCTGTAATGAGACCCCTTCATATCT
ATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA
GCTAAAGTAACGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAAT
CAGGAATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGAAG
CACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA
GAAGCACATAAAGTCGAAGAAGCACCGTAAAGCTGAAGAGGGACATAAAA
CCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTAT
CAAAGTACTACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGT
TTCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATC
AGACACATGTTG

SEQ ID NO. 5109

STRAIN JM9130013

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAAC
CTTACTTAAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGC
TGGAAAAAATTACTTTCAAAGTTTCAAGGATACTGGCATTGGTTTGAAAGA
CGTTTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAG
ACCTTATCACACCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAA
CCAAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAAT
GAGAAGTTTTGATTATTCAACCCACCGGGAACCTAAGCCAAGCAAACCCA
AAGATAGTTTATCAACTCCTCCAGGTTTCCAGATTAAACACGCGCGCG
GATGAAGCACCAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGG
AGCAATTAAATAGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTTA
TTTTAGCTAGCAAAGTAAATGGCAAAATATTACAAGTCAATCTGATGGC
AAATTAGTCATTCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACAC
TAGTCTTAAATTTATCGTAATAATAATCGCAATAAAGAAATTAATATCA
CAACAGATTATTTGAGATACAAAATATGTCAATATCACAGCGGTTGAC
TATTTGAGCAaTACTACTTTTGGAGCAATTAGCTACTGGTGAAACAGTAGA
TTACCAGTCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTG
GTAAGATTTATGTTAAGGATAAATTGCAAGAACTTCTCGTATAGCGCTT
AAAGATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACA
TATTGATAGTTTATCTGTTCTGTTGAAATGAGGTTAAACTGTTGATA
ATATCTTGA AAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAA
TTAAATACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACAT
TAACTCAAGTTTCAAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAG
AATTGGTTGAACAAAAGATGTTTCTTTGGATATAAACGATATGGACATG
AGTAAGTTTAAACTATTTCGACTTGGACGAAAGGATTCTGAATTTAAGGG

Table 51: Comparative Sequences relating to SAG0677

ACAACTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTTCAAAC
 AATCTCAAGACCCAGCTTCAATTATTAATAAAGATGCAATTAACCTTAAAT
 GGTGTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGA
 AAGTCAGATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAAT
 TTAAATTAACCAAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAA
 GATCCATATAGTCATCAGAAAGAAGATATGACTAAAArAGGTGAACAGCT
 CAGTCATTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTA
 ATATTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTT
 GGTAAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTGTATT
 ACATAAAACAGAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGG
 GTAGTGTAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTAGATTATCT
 AAAAATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGC
 GTATTACGAAACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAG
 ATACTAACTTAATTTTAAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAA
 AATATGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGT
 TAGTGAACATAAATACCCATCAGTATTTCTCTTAACCTCTGCCTTATTGG
 AAAGTCTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGT
 ATTATCGGTACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAA
 AATGGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAG
 GTAAAGACTTGACTAATCGAACAAAACCTTAATGAGTGGACGTAGAGTA
 CTTTATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCG
 TTTTAAACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGaGaaag
 cAaGTATTGTTTCGTGCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAAC
 ACAGCAGTTGCTAAACGTGATTGACTTCTGATACTGCTCTTATCCACAT
 CGTTGCCAAAGATGACTCTCTAAACTAAAATTATATCAAGATGATTCAT
 TACTTGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTA
 GAAATCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTAT
 TAAGTTATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTC
 ATATCTATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGAC
 AAAGGAGCTAAAGTAAGTGTGGATATGTTGATGAAGCACTTAGTTGTTCC
 AGAAATGGCAGGAGCTTATACATTAAACAATCGACGAAGCTCCAAACACAA
 ATGAATCAGGAATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAAAT
 GGTGGTGTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGC
 TATTCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTG
 AAGAAGCACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAA
 GCTGAAGAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAGGGAC
 ATAAAACCCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAGGTTAATAAC
 GTTCATCAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAA
 GACAGTTTCCGCAGTTTATATGGCTAGAACAGACAATAAACAGATAACTT
 CACATCAGACACATGTTG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa235280.2{*} December 10, 2002 05:12 ..

	1				50
msa235280.2{195_COH1}	ttgaataata	aaggtgtcgg	tggcgaTGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_M732}	ttgaataata	aaggtgtcgg	tggcgaTGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_M781}	ttgaataata	aaggtgtcgg	tggcgaTGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_H36B}	-----	-----	-----TGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_JM9130013}	-----	-----	-----TGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_18RS21}	ttgaataata	aaggtgtcgg	tggcgaTGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_2603}	ttgaataata	aaggtgtcgg	tggcgaTGGT	GTCCAAATTT	ATCAATACTA
msa235280.2{195_A909}	ttgaataata	aaggtgtcgg	tggcgaTGGT	GTCCAAATTT	ATCAATACTA
Consensus	-----	-----	-----****	*****	*****
	51				100
msa235280.2{195_COH1}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_M732}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_M781}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_H36B}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_JM9130013}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_18RS21}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_2603}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
msa235280.2{195_A909}	TATCAAAATG	GACAACAATA	AACCTTACTT	AAGTCCCAA	GATAAGACTA
Consensus	*****	*****	*****	*****	*****
	101				150
msa235280.2{195_COH1}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_M732}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_M781}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_H36B}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_JM9130013}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_18RS21}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_2603}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
msa235280.2{195_A909}	CTGTAGAGAA	GTTAGAAGAT	CGCTGGAAAA	AAATTACTTT	CAAAGTTCAG
Consensus	*****	*****	*****	*****	*****
	151				200
msa235280.2{195_COH1}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_M732}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_M781}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_H36B}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_JM9130013}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_18RS21}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_2603}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_A909}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M732}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M781}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_H36B}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_JM9130013}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_18RS21}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_2603}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_A909}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M732}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M781}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_H36B}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_JM9130013}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_18RS21}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_2603}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_A909}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_M732}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_M781}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_H36B}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_JM9130013}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_18RS21}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_2603}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_A909}	GATTTACCAc	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M732}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M781}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_H36B}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_JM9130013}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_18RS21}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_2603}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_A909}	GGGAACCTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M732}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M781}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_H36B}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACtAAAGG	ATAGTAAAAA
msa235280.2{195_JM9130013}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_18RS21}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_2603}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_A909}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACtAAAGG	ATAGTAAAAA
Consensus	*****	*****	*****	..***..*****	*****
msa235280.2{195_COH1}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M732}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M781}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_H36B}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_JM9130013}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_18RS21}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_2603}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_A909}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M732}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M781}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_H36B}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_JM9130013}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_18RS21}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_2603}	AACCTAGCTT	TGTTGATGgC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_A909}	AACCTAGCTT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
Consensus	*****	*****	*****	*****	*****

Table 51: Comparative Sequences relating to SAG0677

		551					600
msa235280.2	{195_COH1}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_M732}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_M781}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_H36B}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_JM9130013}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_18RS21}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_2603}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
msa235280.2	{195_A909}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCCTA	GAAATGCTTT	
Consensus		*****	*****	*****	*****	*****	
		601					650
msa235280.2	{195_COH1}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_M732}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_M781}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_H36B}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_JM9130013}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_18RS21}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_2603}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
msa235280.2	{195_A909}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA	
Consensus		*****	*****	*****	*****	*****	
		651					700
msa235280.2	{195_COH1}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_M732}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_M781}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_H36B}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_JM9130013}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_18RS21}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_2603}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
msa235280.2	{195_A909}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA	
Consensus		*****	*****	*****	*****	*****	
		701					750
msa235280.2	{195_COH1}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_M732}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_M781}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_H36B}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_JM9130013}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_18RS21}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_2603}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
msa235280.2	{195_A909}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA	
Consensus		*****	*****	*****	*****	*****	
		751					800
msa235280.2	{195_COH1}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_M732}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_M781}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_H36B}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_JM9130013}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_18RS21}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_2603}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
msa235280.2	{195_A909}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT	
Consensus		*****	*****	*****	*****	*****	
		801					850
msa235280.2	{195_COH1}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_M732}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_M781}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_H36B}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_JM9130013}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_18RS21}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_2603}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
msa235280.2	{195_A909}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTtAA	CGATAAATTG	
Consensus		*****	*****	*****	*****	*****	
		851					900
msa235280.2	{195_COH1}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_M732}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_M781}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_H36B}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_JM9130013}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_18RS21}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_2603}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
msa235280.2	{195_A909}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT	
Consensus		*****	*****	*****	*****	*****	
		901					950
msa235280.2	{195_COH1}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT	
msa235280.2	{195_M732}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT	
msa235280.2	{195_M781}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT	
msa235280.2	{195_H36B}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT	
msa235280.2	{195_JM9130013}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT	

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_18RS21}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGT
msa235280.2{195_2603}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGT
msa235280.2{195_A909}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGT
Consensus	*****	*****	*****	*****	*****
951					
msa235280.2{195_COH1}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M732}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M781}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_H36B}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_JM9130013}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_18RS21}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_2603}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_A909}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
Consensus	*****	*****	*****	*****	*****
1001					
msa235280.2{195_COH1}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M732}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M781}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_H36B}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_JM9130013}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_18RS21}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_2603}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_A909}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
Consensus	*****	*****	*****	*****	*****
1051					
msa235280.2{195_COH1}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M732}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M781}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_H36B}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_JM9130013}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_18RS21}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_2603}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_A909}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
Consensus	*****	*****	*****	*****	*****
1101					
msa235280.2{195_COH1}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M732}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M781}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_H36B}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_JM9130013}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_18RS21}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_2603}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_A909}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
Consensus	*****	*****	*****	*****	*****
1151					
msa235280.2{195_COH1}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_M732}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_M781}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_H36B}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_JM9130013}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_18RS21}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_2603}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
msa235280.2{195_A909}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTTCGACTTG
Consensus	*****	*****	*****	*****	*****
1201					
msa235280.2{195_COH1}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M732}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M781}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_H36B}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_JM9130013}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_18RS21}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_2603}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_A909}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
Consensus	*****	*****	*****	*****	*****
1251					
msa235280.2{195_COH1}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M732}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M781}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_H36B}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_JM9130013}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_18RS21}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_2603}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_A909}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
Consensus	*****	*****	*****	*****	*****
1301					
1350					

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_COH1}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_M732}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_M781}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_H36B}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_JM9130013}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_18RS21}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_2603}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_A909}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
Consensus	*****	*****	*****	*****	*****
1351					
msa235280.2{195_COH1}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_M732}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_M781}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_H36B}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_JM9130013}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_18RS21}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_2603}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_A909}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
Consensus	*****	*****	*****	*****	*****
1401					
msa235280.2{195_COH1}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_M732}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_M781}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_H36B}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_JM9130013}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_18RS21}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_2603}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
msa235280.2{195_A909}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAGTGG	TGCAAGTCTT
Consensus	*****	*****	*****	*****	*****
1451					
msa235280.2{195_COH1}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_M732}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_M781}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_H36B}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_JM9130013}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_18RS21}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_2603}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_A909}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
Consensus	*****	*****	*****	*****	*****
1501					
msa235280.2{195_COH1}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_M732}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_M781}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_H36B}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_JM9130013}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_18RS21}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_2603}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
msa235280.2{195_A909}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAATGAAA
Consensus	*****	*-*****	*****	*****	*****
1551					
msa235280.2{195_COH1}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_M732}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_M781}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_H36B}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_JM9130013}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_18RS21}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_2603}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_A909}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
Consensus	*****	*****	*****	*****	*****
1601					
msa235280.2{195_COH1}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_M732}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_M781}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_H36B}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_JM9130013}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_18RS21}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_2603}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_A909}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
Consensus	*****	*****	*****-*****	*****	*****
1651					
msa235280.2{195_COH1}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_M732}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_M781}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_H36B}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_JM9130013}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_18RS21}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_2603}	TAAAGGATGG	ACAACATTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_A909}	TAAAGGATGG	ACAACATTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
Consensus	*****	*****	*****	*****	*****
1701					
msa235280.2{195_COH1}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_M732}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_M781}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_H36B}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_JM9130013}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_18RS21}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_2603}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_A909}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
Consensus	*****	*****	*****	*****	*****
1751					
msa235280.2{195_COH1}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M732}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M781}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_H36B}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_JM9130013}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_18RS21}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_2603}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_A909}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
Consensus	*****	*****	*****	*****	*****
1801					
msa235280.2{195_COH1}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M732}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M781}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_H36B}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_JM9130013}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_18RS21}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_2603}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_A909}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
Consensus	*****	*****	*****	*****	*****
1851					
msa235280.2{195_COH1}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M732}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M781}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_H36B}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_JM9130013}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_18RS21}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_2603}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_A909}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
Consensus	*****	*****	*****	*****	*****
1901					
msa235280.2{195_COH1}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_M732}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_M781}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_H36B}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_JM9130013}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_18RS21}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_2603}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
msa235280.2{195_A909}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCAGT
Consensus	*****	*****	*****	*****	*****
1951					
msa235280.2{195_COH1}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M732}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M781}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_H36B}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_JM9130013}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_18RS21}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_2603}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_A909}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
Consensus	*****	*****	*****	*****	*****
2001					
msa235280.2{195_COH1}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M732}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M781}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_H36B}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_JM9130013}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_18RS21}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_2603}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_A909}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
Consensus	*****	*****	*****	*****	*****
2051					
msa235280.2{195_COH1}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
2100					

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M732}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_M781}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_H36B}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_JM9130013}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_18RS21}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_2603}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_A909}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M732}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M781}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_H36B}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_JM9130013}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_18RS21}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_2603}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_A909}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_M732}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_M781}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_H36B}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_JM9130013}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_18RS21}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_2603}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_A909}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TCGAACAAAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M732}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M781}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_H36B}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_JM9130013}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_18RS21}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_2603}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_A909}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_M732}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_M781}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_H36B}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_JM9130013}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_18RS21}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_2603}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_A909}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M732}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M781}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_H36B}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_JM9130013}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_18RS21}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_2603}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_A909}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M732}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M781}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_H36B}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_JM9130013}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_18RS21}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_2603}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_A909}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M732}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M781}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_H36B}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_JM9130013}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_18RS21}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_2603}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_A909}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
Consensus	*****	*****	*****	*****	*****
	2451				2500
msa235280.2{195_COH1}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_M732}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_M781}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_H36B}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_JM9130013}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_18RS21}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_2603}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_A909}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
Consensus	*****	*****	*****	*****	*****
	2501				2550
msa235280.2{195_COH1}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_M732}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_M781}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_H36B}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_JM9130013}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_18RS21}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_2603}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_A909}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
Consensus	*****	*****	*****	*****	*****
	2551				2600
msa235280.2{195_COH1}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_M732}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_M781}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_H36B}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_JM9130013}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_18RS21}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_2603}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_A909}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
Consensus	*****	*****	***-*****	*****	*****
	2601				2650
msa235280.2{195_COH1}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_M732}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_M781}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_H36B}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_JM9130013}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_18RS21}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_2603}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_A909}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
Consensus	*****	*****	*****	*****	*****
	2651				2700
msa235280.2{195_COH1}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_M732}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_M781}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_H36B}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_JM9130013}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_18RS21}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_2603}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_A909}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
Consensus	*****	*****	*****	*****	*****
	2701				2750
msa235280.2{195_COH1}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_M732}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_M781}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_H36B}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_JM9130013}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_18RS21}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_2603}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_A909}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
Consensus	*****	*****	*****	*****	*****
	2751				2800
msa235280.2{195_COH1}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_M732}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_M781}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_H36B}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_JM9130013}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_18RS21}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_2603}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_A909}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
Consensus	*****	**-*****	*****	*****	*****
	2801				2850
msa235280.2{195_COH1}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_M732}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M781}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_H36B}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_JM9130013}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_18RS21}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_2603}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_A909}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M732}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M781}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_H36B}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_JM9130013}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_18RS21}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..
msa235280.2{195_2603}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..
msa235280.2{195_A909}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
Consensus	*****	*****	*****	-----	-----
msa235280.2{195_COH1}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M732}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M781}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_H36B}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_JM9130013}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_18RS21}CGTAAAGC	TGAaGAAGCA
msa235280.2{195_2603}cgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_A909}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
Consensus	-----	-----	-----	-----	-----
msa235280.2{195_COH1}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M732}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M781}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_H36B}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_JM9130013}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_18RS21}	CgTAAAGCTG	AAGAAGcA..
msa235280.2{195_2603}	CgTAAAGCTG	AAGAAGcA..
msa235280.2{195_A909}	CgTAAAGCTG	AAGAAGcA..
Consensus	*-*****	*****-*	-----	-----	-----
msa235280.2{195_COH1}	agca.CGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M732}	agca.CGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M781}	agcacCGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_H36B}	agca.CGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_JM9130013}	agcacCGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_18RS21}CGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_2603}CGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_A909}CGTAAGCTG	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
Consensus	-----	*****	*****	*****	*****
msa235280.2{195_COH1}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_M732}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_M781}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_H36B}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_JM9130013}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_18RS21}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_2603}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
msa235280.2{195_A909}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAACTGATA	CTACAGTTAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M732}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M781}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_H36B}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_JM9130013}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_18RS21}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_2603}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_A909}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	-----
msa235280.2{195_M732}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAA-----
msa235280.2{195_M781}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_H36B}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	-----
msa235280.2{195_JM9130013}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_18RS21}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAA-----
msa235280.2{195_2603}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA
msa235280.2{195_A909}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA

Table 51: Comparative Sequences relating to SAG0677

Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	3201				3250
msa235280.2{195_M732}					
msa235280.2{195_M781}					
msa235280.2{195_H36B}					
msa235280.2{195_JM9130013}					
msa235280.2{195_18RS21}					
msa235280.2{195_2603}	ATTAAAAATA	cattgccatc	cactgggtgac	agcaaacgtg	gttattatat
msa235280.2{195_A909}	ATTAAAAATA				
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	3251				3300
msa235280.2{195_M732}					
msa235280.2{195_M781}					
msa235280.2{195_H36B}					
msa235280.2{195_JM9130013}					
msa235280.2{195_18RS21}					
msa235280.2{195_2603}	cactggaatg	gctatcgtta	tgctgagtg	attatttagt	ttagctaaaa
msa235280.2{195_A909}					
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	3301	3317			
msa235280.2{195_M732}					
msa235280.2{195_M781}					
msa235280.2{195_H36B}					
msa235280.2{195_JM9130013}					
msa235280.2{195_18RS21}					
msa235280.2{195_2603}	agtttaaaag	caaatat			
msa235280.2{195_A909}					
Consensus	*****	*****			

SEO ID NO. 5110

STRAIN 2603 frame: 1

LNNKGVGGDGVQIYQYYIKMDNNKPYLSPDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDGPILASKV
NGKILQVESDQGLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNI
TAVDYLNTTTFEQLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLQNETSRIALAKDKSVKIGI
ELPNDVRHIDSLSVRRNLNEVKTVDNINLKNDEQDINLSKTYQLKYNTNRRLFTINNINS
SSEIMTTFKDGKMPELVEQKDVSLDINDMDSKFKTIRLGRKDSEFKGQLIAKTGTVELD
MFFKQSQDPASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS
ASLKVVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
VVKGSELPLTKGWTFVLHKTENSLNVKSLIMETGVSVKVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLLTALLETASEATLNGKEITASGIIHIGDGDKSKHVEVKMVNENGDMGLGTP
VI IQGKDLTNRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTENGEGAKSI
VRRMFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDM
LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVISIHYVNGGVDKVDVPIKVVDLEAIR
KAE EARKAE EARKAE EARKAE EGHKTQEAPIVEEGYKVVNNVHQTDTTVKASDLPKTKTVS
AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYYITGMAIVMLSVLFSLAKKFKSK
Y

SEO ID NO. 5111

STRAIN A909 frame: 1

LNNKGVGGDGVQIYQYYIKMDNNKPYLSPDKDTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEPKLDRPPGIDLPPPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEALKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
NGKILQVESDGGKGLVIRNALNSANQFDDTSLKIRYNNNRNKEITITTDYFADTKYVNITAV
DYLNTTTFEQLATGETVYHAIVFSFAAIKDGKGIYVNDKLQETSRIALKQDSVKIGI
ELPNDVRHIDLSVRRRLNEVKTVDNILKNDEQDINLSKTFYQLKYNPTNRRLLEFTINNINS
SSEIMTTTFKDGKMPELVEQKDVSLDINDMDSKFKTIRLGRKDESEFKGQLIAKTGTVELD
MFFKQSQDPASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTSG
ASLKVVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
VGKGSSELPLTKGWTTFVLHKTENSINVKSLIMETGVSVKVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVRILNLTADTKLNFNAVKGASALTENMMMRQFVAVAGQDDPVS
HKYPSVFLLTPALLETASEATLNGKEITASGIIHIGIKDGDKSKHVEVKVMNENGDMLGTP
VIIQGKDLTNRTKPLMSGRRVLAYAGQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
VEITKDMTVPLEFGDNIILKSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDM
LMKHLVVPEMAGAYTLTIDEDPNTNESGMLTNAKVISIHYVNGGVDKVDVPIKVVdleAIR
KAEAEHKADEARKAEARKAEARKAEARKAEAEHGHKTQEAPIVEEGYKVVNVHQTDTTV
KASDLPKTKTVSAVHMARTDNKOITSHOOTHVEKOIKN

SEQ ID NO. 5112

STRAIN H36B frame: 2

GVQIYQYYIKMDNNKPYLSPDKKTVEKLEDRWKKITFKVQDTGIGLKDVYLSVKYVGG
GNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTPKSPKPKDSLS
TPPGFPDLNTPPDEALKDSSKDAIEDKSGAIKYAKSLLSFVDDPILASKVNGKILOVES

Table 51: Comparative Sequences relating to SAG0677

DGKLVI PRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAVDYLSTNTTFF
 QLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALDKDSVKIGIELPNDVRHI
 DLSVRRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINSSSEIMTTFK
 DGKMPPELVEQKDVSLDINDMDMSKFKTIRLGRKDESEFKGQLIAKTGTVELDMFFKQSQDP
 ASI IKKIYLIQNGVNPENLKKFDSSFGLTESQIDGYIYKDAILNKFCLTSGASLKVYK
 QEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKEVGKSELPL
 TKGWTTFFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDMLLTMQKDSAY
 YETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSEHKYPSVFL
 TPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTPVVIQKDLT
 NRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVTEAGEKASIVRRMFFDQSVPE
 INTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNGVEITKDMTV
 PLEFGDNITKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDMLMKHLVPE
 MAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIRKAEAAHKA
 EARKAEAEARKADEAHKAEVRAKAEAAHKEVEARKAEAGHKTQEAPIVEEGYKVN NVHQTD
 TTVKASDLPKTKTVSAVHMARTDNKQITSHQTH

SEQ ID NO. 5113

STRAIN 18RS21 frame: 1

LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
 VY LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
 TK PSKPKDSLSTPPGFPDLNTPDEAPKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAV
 DYLSTNTTFFQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALDKDSVKIGI
 ELPNDVRHIDLSVRRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNIN
 SSESIMTTFKDGKMPPELVEQKDVSLDINDMDMSKFKTIRLGRKDESEFKGQLIAKTGTVEL
 DMFFKQSQDPASI IKKIYLIQNGVNPENLKKFDSSFGLTESQIDGYIYKDAILNKFCLTSG
 ASLKVYKQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
 VVGKSELPLTKGWTTFFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
 HKYPSVFLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTP
 VVIQKDLTNRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVTEAGEKASIVRR
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
 VEITKDMTVPLEFGDNITKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDML
 MKHLVPEMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR
 KAEAEARKAEAEARKAEAGHKTQEAPIVEEGYKVN NVHQTD TTVKASDLPKTKTVSAVHMAR
 TDNKQITSHQTHVE

SEQ ID NO. 5114

STRAIN M732 frame: 1

LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
 VY LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
 TK PSKPKDSLSTPPGFPDLNTPDEATKG. KRRY. R. IRSN. IC. VSST. LC. PYFS. QS
 KWQNTSRI. WQISHS. KCFVS. SI. H. S. NLS. . SQ. RNYHNLFCRYKICQYHSG
 . LFEQYF. AISYW. NSRLPCHCIFKLCCY. RQGW. DLC. R. IARNFSYSA. R. IC. DWY
 . ITK. CQTY. . FICSSFE. G. NC. . YLEK. . TRH. SQQNLPIKI QPDKSSSRVYY. . H. L
 KFRNHDHFQRWKDARIG. TKRCFFGYKRYGHE. V. NYSTWTKGF. I. GTTYCKNWS. IR
 YVFQTSRPSFNY. KNIPYPKWCSK. IEKI. L. FWFN. KSDRWILYL. RCN. P. I. INQW
 CKS. SCL. RARRSI. SSERRYD. KR. TAQSFNSSQ. KYSKSNLC. Y. LVTL. . GYCEWKR
 SW. R. . VTFN. RMDNICIT. NRKFIK. KFDYGDG. CK. ESSTTSFKS. II. K. AYEGLA
 TTYAKRFSVLNRK. QSSPSN. SHCRY. T. F. CC. RSECSY. KYDDETVCSCTWTR. SC. .
 T. IPISISLNSCLIGNC. . GNSKW. GNHSIWYRSHQGW. . KQAC. SQNGE. KWRHARNP
 CYYSR. RLD. SNKTINWT. STLCT. TI. VPG. ITT. SF. HLD. G. SGNRSRRESKYCSS
 HVL. PISSRA. HSSC. T. FDF. YCSYPHRCQR. LSKTKIISR. FIT. IC. . NRSL. F. KW
 CRNH. RYDSTTRIWR. YY. VICC. LIKLSS. . DPSYL. KPF. C. SKPND. QRS. SNCGY
 VDEALSCSRNGRSLYINNRRSSKHK. IRNVNKR. SIDLCKWWC. . S. CSD. SS. LRSYS
 . S. RST. S. RST. S. RST. S. RST. S. RST. S. RST. SRRST. S. RGT. NPRSTYS. RRL
 QS. . RSSN. YYS. SV. FTKD. DSFRSSYG. NRQ. TDNFTSDTC. K

SEQ ID NO. 5115

STRAIN COH1 frame: 1

LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
 VY LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
 TK PSKPKDSLSTPPGFPDLNTPDEATKG. KRRY. R. IRSN. IC. VSST. LC. PYFS. QS
 KWQNTSRI. WQISHS. KCFVS. SI. H. S. NLS. . SQ. RNYHNLFCRYKICQYHSG
 . LFEQYF. AISYW. NSRLPCHCIFKLCCY. RQGW. DLC. R. IARNFSYSA. R. IC. DWY
 . ITK. CQTY. . FICSSFE. G. NC. . YLEK. . TRH. SQQNLPIKI QPDKSSSRVYY. . H. L
 KFRNHDHFQRWKDARIG. TKRCFFGYKRYGHE. V. NYSTWTKGF. I. GTTYCKNWS. IR
 YVFQTSRPSFNY. KNIPYPKWCSK. IEKI. L. FWFN. KSDRWILYL. RCN. P. I. INQW
 CKS. SCL. RARRSI. SSERRYD. KR. TAQSFNSSQ. KYSKSNLC. Y. LVTL. . GYCEWKR
 SW. R. . VTFN. RMDNICIT. NRKFIK. KFDYGDG. CK. ESSTTSFKS. II. K. AYEGLA
 TTYAKRFSVLNRK. QSSPSN. SHCRY. T. F. CC. RSECSY. KYDDETVCSCTWTR. SC. .
 T. IPISISLNSCLIGNC. . GNSKW. GNHSIWYRSHQGW. . KQAC. SQNGE. KWRHARNP
 CYYSR. RLD. SNKTINWT. STLCT. TI. VPG. ITT. SF. HLD. G. SGNRSRRESKYCSS
 HVL. PISSRA. HSSC. T. FDF. YCSYPHRCQR. LSKTKIISR. FIT. IC. . NRSL. F. KW
 CRNH. RYDSTTRIWR. YY. VICC. LIKLSS. . DPSYL. KPF. C. SKPND. QRS. SNCGY
 VDEALSCSRNGRSLYINNRRSSKHK. IRNVNKR. SIDLCKWWC. . S. CSD. SS. LRSYS
 . S. RST. S. RST. S. RST. S. RST. S. RST. S. RST. SRRST. S. RGT. NPRSTYS. RRL
 QS. . RSSN. YYS. SV. FTKD. DSFRSSYG. NRQ. TDNFTSDTC

SEQ ID NO. 5116

STRAIN M781 frame: 1

LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
 VY LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
 TK

Table 51: Comparative Sequences relating to SAG0677

PSKPKDLSLSTPPGFDLNTPPDEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNITSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYHNRLFRCRYKICQYHSG
.LFEQYQYF.AISYW.NSRLPGCHCIFKLCCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQNLPIKIQDPKSSSRVYY..H.L
KFRNHDHFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.J.GTTYCKNWSN.IR
YVFQTIISRPSFNY.KNIPYPKWCSK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIKC.KFDYGDG.CK.ESSTTSFKS.II.K.AYEGYA
TYYAKRFSVLNRN.QSSPSN.SHCRY.T.F.CC.RSECSY.KYDDETVCSWITR.SC..
T.IPISISLNSCLIGNC..GNSKG.GNHSIWYYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.ITT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCQR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPND.S.QRS.SNCGY
VDEALSCSRNGRSLYINNRSSKHK.IRNVNKR.SIDSLCKWNC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRSTVKLRDIPKPKHL.LKKA
TKLITFIKLILQLKRLIYQRLRQFPQFIWLEQTINR.LHIRHML

SEQ ID NO. 5117

STRAIN JM9130013 frame: 2

GVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVYLQSVKYVGG
GNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTPKPSKPKDSLS
TPPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES
DGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNIATAVDLSNTTFE
QLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKQLTQTSRIALDKDSVKIGIELPNDVRHI
DLSVRRNLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINSSSEIMTTFK
DGKMPELVEQKDVSLDINDMDMSKFKTIRLGRKDSEFKGQLIAKTGTVELDMFFKQSQDP
ASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTSGASLKVVYKG
QEDPYSHQKEDMTKXGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKEVGKGSSELPL
TKGWTITFVLHKTENSLNVKSLIMETGVSVKVQQLPLSPRLSKNKHMRDMLHTMQKDSAY
YETSDSLVLRINLTADTKLNFNAVKGSALIENTENMMMRQFAVAGQDDFVSEHKTSPSVFL
TPALLETASEATLNGKEITASGIIIGHIKDGDKSKHVEVKMVNENGDMLGTPVIIQGKDLT
NRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRRMFFDQSVPE
LNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNGVEITKDMTV
PLEFGDNI IKLSAVDLSNYNRNETLHIYRNRFVDVKASQMTADGKAKVTVDMLMKHLVPE
MAGAYTLTIDEAPNTNESGMLTNAKVS IHYVNGGVDKVDVPIKVVDLEAIRKAEAAHKAD
EARKAEARKAEAAHKAEVRKAEAAHKVEAP.S.RGT.NPRSTYS.RRLQG..RSSN.
YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

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PRETTY of: /biotmp/msa235427.2{*}    December 10, 2002 05:18  ..
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	1		50
msa235427.2{195_H36B}	-----G	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_JM9130013}	-----G	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_18RS21}	LNNKGVGVDG	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_2603}	LNNKGVGVDG	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_A909}	LNNKGVGVDG	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_COH1}	LNNKGVGVDG	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_M732}	LNNKGVGVDG	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_M781}	LNNKGVGVDG	VQIYQYYIKM	DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
Consensus	*****	*****	*****

	51	100
msa235427.2{195_H36B}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_JM9130013}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_18RS21}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_2603}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_A909}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_COH1}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_M732}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_M781}	DTGIGLKD VY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
Consensus	*****	*****

		101				150
msa235427.2{195_H36B}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEAlKdskK	
msa235427.2{195_JM9130013}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEApKdskK	
msa235427.2{195_18RS21}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEApKdskK	
msa235427.2{195_2603}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEApKdskK	
msa235427.2{195_A909}	DLpPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEAlKdskK	
msa235427.2{195_COH1}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEAtKg. .K	
msa235427.2{195_M732}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEAtKg. .K	
msa235427.2{195_M781}	DLPaPTSMRS	FDYSTPPG	PSKPKDSL	PPGF	PDEAtKg. .K	
	Consensus	*****	*****	*****	*****	*****

	151		200
msa235427.2{195_H36B}	daiedksgai	kyakslqlsf	vddPilaskv ngkilqvesd gklviprnal
msa235427.2{195_JM9130013}	daiedksgai	kyakslqlsf	vddPilaskv ngkilqvesd gklviprnal
msa235427.2{195_18RS21}	daiedksgai	kyakslqlsf	vddPilaskv ngkilqvesd gklviprnal
msa235427.2{195_2603}	daiedksgai	kyakslqlsf	vdgPilaskv ngkilqvesd gklviprnal
msa235427.2{195_A909}	daiedksgai	kyakslqlsf	vddPilaskv ngkilqvesd gklviprnal
msa235427.2{195_COH1}	rry.r.irsn	.ic.vsst.1	c..Pyfs.qs kwqnitsri.wqishs.kcf
msa235427.2{195_M732}	rry.r.irsn	.ic.vsst.1	c..Pyfs.qs kwqnitsri.wqishs.kcf
msa235427.2{195_M781}	rry.r.irsn	.ic.vsst.1	c..Pyfs.qs kwqnitsri.wqishs.kcf
Consensus	-----	-----	*-----

Table 51: Comparative Sequences relating to SAG0677

	201			250
msa235427.2{195_H36B}	sanqfddtsl	kiyrnnnrnk	eititttdyFa	dtKyvmitav dylsnttFeq
msa235427.2{195_JM9130013}	sanqfddtsl	kiyrnnnrnk	eititttdyFa	dtKyvmitav dylsnttFeq
msa235427.2{195_18RS21}	sanqfddtsl	kiyrnnnrnk	eititttdyFa	dtKyvmitav dylsnttFeq
msa235427.2{195_2603}	sanqfddtsl	kiyrnnnrnk	eititttdyFa	dtKyvmitav dylsnttFeq
msa235427.2{195_A909}	sanqfddtsl	kiyrnnnrnk	eititttdyFa	dtKyvmitav dylsnttFeq
msa235427.2{195_COH1}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq .lfeqyyF.a
msa235427.2{195_M732}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq .lfeqyyF.a
msa235427.2{195_M781}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq .lfeqyyF.a
Consensus	-----	-----	-----*	-----*
	251			300
msa235427.2{195_H36B}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria lkdksvkigi
msa235427.2{195_JM9130013}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria lkdksvkigi
msa235427.2{195_18RS21}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria lkdksvkigi
msa235427.2{195_2603}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria lkdksvkigi
msa235427.2{195_A909}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria lkdksvkigi
msa235427.2{195_COH1}	isyw.nsrlp	chcifklccy	.rqGw.dlc.	r.iarnfsys a.r.ic.dwy
msa235427.2{195_M732}	isyw.nsrlp	chcifklccy	.rqGw.dlc.	r.iarnfsys a.r.ic.dwy
msa235427.2{195_M781}	isyw.nsrlp	chcifklccy	.rqGw.dlc.	r.iarnfsys a.r.ic.dwy
Consensus	-----	-----	-----*	-----
	301			350
msa235427.2{195_H36B}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty qlKynPtnrr
msa235427.2{195_JM9130013}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty qlKynPtnrr
msa235427.2{195_18RS21}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty qlKynPtnrr
msa235427.2{195_2603}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty qlKynPtnrr
msa235427.2{195_A909}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty qlKynPtnrr
msa235427.2{195_COH1}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqqnl piKiqPdkss
msa235427.2{195_M732}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqqnl piKiqPdkss
msa235427.2{195_M781}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqqnl piKiqPdkss
Consensus	-----	-----	-----*	-----*
	351			400
msa235427.2{195_H36B}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd mskfktirlg
msa235427.2{195_JM9130013}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd mskfktirlg
msa235427.2{195_18RS21}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd mskfktirlg
msa235427.2{195_2603}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd mskfktirlg
msa235427.2{195_A909}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd mskfktirlg
msa235427.2{195_COH1}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg he.v.nystw
msa235427.2{195_M732}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg he.v.nystw
msa235427.2{195_M781}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg he.v.nystw
Consensus	-----	-----*	-----*	-----
	401			450
msa235427.2{195_H36B}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq ngvpnelkKf
msa235427.2{195_JM9130013}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq ngvpnelkKf
msa235427.2{195_18RS21}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq ngvpnelkKf
msa235427.2{195_2603}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq ngvpnelkKf
msa235427.2{195_A909}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq ngvpnelkKf
msa235427.2{195_COH1}	tKgfi.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp kwcsk.ieKi
msa235427.2{195_M732}	tKgfi.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp kwcsk.ieKi
msa235427.2{195_M781}	tKgfi.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp kwcsk.ieKi
Consensus	-----*	-----*	-----*	-----*
	451			500
msa235427.2{195_H36B}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvkygq edpyshqked
msa235427.2{195_JM9130013}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvkygq edpyshqked
msa235427.2{195_18RS21}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvkygq edpyshqked
msa235427.2{195_2603}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvkygq edpyshqked
msa235427.2{195_A909}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvkygq edpyshqked
msa235427.2{195_COH1}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra rrsi.sserr
msa235427.2{195_M732}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra rrsi.sserr
msa235427.2{195_M781}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra rrsi.sserr
Consensus	-----*	-----	-----	-----
	501			550
msa235427.2{195_H36B}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe vgkgselplt
msa235427.2{195_JM9130013}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe vgkgselplt
msa235427.2{195_18RS21}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe vgkgselplt
msa235427.2{195_2603}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe vgkgselplt
msa235427.2{195_A909}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe vgkgselplt
msa235427.2{195_COH1}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr sw.r..vtfn
msa235427.2{195_M732}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr sw.r..vtfn
msa235427.2{195_M781}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr sw.r..vtfn
Consensus	-----	-----*	-----	-----*
	551			600
msa235427.2{195_H36B}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl sknkhmrdbl
msa235427.2{195_JM9130013}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl sknkhmrdbl
msa235427.2{195_18RS21}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl sknkhmrdbl
msa235427.2{195_2603}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl sknkhmrdbl

Table 51: Comparative Sequences relating to SAG0677

msa235427.2{195_A909}	kgwtttfvlhk	tenslnvksl	imetGavskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_COH1}	.rmdnicit.	nrkfikc.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M732}	.rmdnicit.	nrkfikc.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M781}	.rmdnicit.	nrkfikc.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	lTmqkdsayy	etsdsllvri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_JM9130013}	lTmqkdsayy	etsdsllvri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_18RS21}	lTmqkdsayy	etsdsllvri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_2603}	lTmqkdsayy	etsdsllvri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_A909}	lTmqkdsayy	etsdsllvri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_COH1}	aTyyakrfsv	lrnk.qssps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M732}	aTyyakrfsv	lrnk.qssps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M781}	aTyyakrfsv	lrnk.qssps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	agpqddpvse	hkypsvflit	pallatasea	tlngkeitaS	giighikdGd
msa235427.2{195_JM9130013}	agpqddpvse	hkypsvflit	pallatasea	tlngkeitaS	giighikdGd
msa235427.2{195_18RS21}	agpqddpvse	hkypsvflit	pallatasea	tlngkeitaS	giighikdGd
msa235427.2{195_2603}	agpqddpvse	hkypsvflit	pallatasea	tlngkeitaS	giighikdGd
msa235427.2{195_A909}	agpqddpvse	hkypsvflit	pallatasea	tlngkeitaS	giighikdGd
msa235427.2{195_COH1}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M732}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M781}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
Consensus	-----	-----	-----*	-----*	-----*
msa235427.2{195_H36B}	ksKhvevkmv	nEngdmlgtp	viigqkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_JM9130013}	ksKhvevkmv	nEngdmlgtp	viigqkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_18RS21}	ksKhvevkmv	nEngdmlgtp	viigqkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_2603}	ksKhvevkmv	nEngdmlgtp	viigqkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_A909}	ksKhvevkmv	nEngdmlgtp	viigqkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_COH1}	..Kqac.sqn	gE.kwrharn	pcyysr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M732}	..Kqac.sqn	gE.kwrharn	pcyysr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M781}	..Kqac.sqn	gE.kwrharn	pcyysr.rld	.snktinewt	.stlcr.ti.
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_JM9130013}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_18RS21}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_2603}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_A909}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_COH1}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M732}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M781}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_JM9130013}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_18RS21}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_2603}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_A909}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_COH1}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	..nrsl.f.k	wcrnh.ryds
msa235427.2{195_M732}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	..nrsl.f.k	wcrnh.ryds
msa235427.2{195_M781}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	..nrsl.f.k	wcrnh.ryds
Consensus	-----	-----*	-----	-----	-----
msa235427.2{195_H36B}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_JM9130013}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_18RS21}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_2603}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_A909}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_COH1}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncg
msa235427.2{195_M732}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncg
msa235427.2{195_M781}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncg
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_JM9130013}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_18RS21}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_2603}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_A909}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_COH1}	yvdealcsr	nGrsl yinnr	rsakhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M732}	yvdealcsr	nGrsl yinnr	rsakhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M781}	yvdealcsr	nGrsl yinnr	rsakhk.irn	vNkr.SIdsl	ckwwc..s.c
Consensus	-----	-----*	-----	-----*	-----

Table 51: Comparative Sequences relating to SAG0677

	951			1000	
msa235427.2{195_H36B}	ikvvdleair	kaeeahkade	arkaeearka	deahkaeevr	kaeeahkvee
msa235427.2{195_JM9130013}	ikvvdleair	kaeeahkade	arkaeearka	eeahkaeevr	kaeeahkvee
msa235427.2{195_18RS21}	ikvvdlea..irkaee	arkaeearka	eeghktqeap	iveegykvnn
msa235427.2{195_2603}	ikvvdleair	kaeearkae	arkaeearka	eeghktqeap	iveegykvnn
msa235427.2{195_A909}	ikvvdleair	kaeeahkade	arkaeearka	eearkaeear	kaeeghktqe
msa235427.2{195_COH1}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M732}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M781}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
Consensus	-----	-----	-----	-----	-----
	1001			1050	
msa235427.2{195_H36B}	arkaeeghkt	qeapiveegy	kvnnvhqtdt	tvkasdlpkt	ktvsavhmar
msa235427.2{195_JM9130013}	ap.s.rgt.n	prstys.rrl	qg..rssn.y	ys.sv.ftkd	.dsfrssyg.
msa235427.2{195_18RS21}	vhqtdttvka	sdlpktktvs	avhmartdnk	qitshqthve	-----
msa235427.2{195_2603}	vhqtdttvka	sdlpktktvs	avhmartdnk	qitshqthve	kqikntlpst
msa235427.2{195_A909}	apiveegykv	nnvhqtdttv	kasdlpktkt	vsavhmartd	nkqitshqth
msa235427.2{195_COH1}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M732}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M781}	rstvklkrdi	kpkkhl.lkk	atklitfikl	ilqlkrliyg	rlrqfpqfiw
Consensus	-----	-----	-----	-----	-----
	1051			1081	
msa235427.2{195_H36B}	tdnkqitshq	th-----	-----	~	
msa235427.2{195_JM9130013}	nrq.tdnfts	dte-----	-----	~	
msa235427.2{195_18RS21}	-----	-----	-----	~	
msa235427.2{195_2603}	gdsrgyyit	gmaivmlsl	fslakkfksk	y	
msa235427.2{195_A909}	vekqikn--	-----	-----	~	
msa235427.2{195_COH1}	.nrq.tdnft	sdTC-----	-----	~	
msa235427.2{195_M732}	.nrq.tdnft	sdTC.k----	-----	~	
msa235427.2{195_M781}	leqtinr.lh	irhml-----	-----	~	
Consensus	-----	-----	-----	~	

Table 52: Comparative Sequences relating to SAG 1823

SEQ ID NO. 5201

STRAIN 090

AGCGATACCTTTTAATTTTGATATTGACCAAATTGCAGA
 CAATGCTATCACTAAAACAGATAAAAACAACAGAAATTATTTCCAACCAGA
 CAACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAACTAACACCAGCA
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
 CGGCGATCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCG
 TTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
 TATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAA
 ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
 TATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCaGCGAA
 TGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAA
 TGCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATT
 GCTTtTATTGAATCgAGTCAAGCCGAGGCTGCTAATCGTgGCAaGCCACTT
 ACAACAAGAAATTCTAGCATTAGATAGCCaAACGTcCGAGTATCAAATtA
 AAAGTaACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAG
 CAACATACTGAATATGTGAGCCGTCTCTACGTTGCATGGGCAACAACACC
 ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAAACTTG
 GCATGTTACGTGCAAAATACCATTTCCAACAATGAAACTCTCAATCGCTCAG
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
 TGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAG
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCaATTGGAATCTG
 CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT
 AAAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAAGAAAA
 AGTTGATGAGTCT

SEQ ID NO. 5202

STRAIN A909

AGCGATACCTTTTAATTTTGATATTGACCAAATTGCAGA
 CAATGCTATCACTAAAACAGATAAAAACAACAGAAATTATTTCCAACCAGA
 CAACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAACTAACACCAGCA
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
 CGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCG
 TTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
 TATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAA
 ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
 TATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAA
 TGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAA
 TGCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTAwT
 GCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTT
 ACAACAAGAAATTCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA
 AAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAG
 CAACATACTGAATATGTGAGCCGTCTCTACGTTGCATGGGCAACAACACC
 ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTG
 GCATGTTACGTGCAAAATACCATTTCCAACaATGAAACTCTCAATCGCTCAG
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
 TGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAG
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCaATTAGAATCTG
 CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT
 AAAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAAGAAAA
 AGtTGATGAGTCT

SEQ ID NO. 5203

STRAIN H36B

AGCGaTACCTTTTAATTTTGATATTGACCAAATTGCAGAC
 AATGCTATCACTAAAACAGATAAAAACAACAGAAATTATTTCCAACCAGAC
 AACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAACTAACACCAGCAC
 AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
 GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCGT
 TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC
 CTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTT
 ATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAA
 CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
 ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT
 GTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTcTCTGCTGAAAT
 GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG
 CTtTATTGAATCGAGTCAAGCCGAgGCTGCCAATCGTGCAAGCCACTTA
 CAACAAGAAATTCTAGCATTAGATAGCCAAACGTcCGAGTATCAAATTAA
 AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAGC
 AACATACTGAATATGTGAGCCGTCTCTACGTTGCATGGGCAACAACACCA
 CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTGG
 CATGTTACGTGCAAAATACCATTTCCAACaATGAAACTCTCAATCGCTCAGT
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
 GTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAGA
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
 AATCTGTCACTGCATTATCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
 ATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGC

Table 52: Comparative Sequences relating to SAG 1823

TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATa
 AAAAAATAGTTGAAGCCTTACTCAaCGAAGGTaAATCTACCCAAGAAAAA
 GTTGATGAGTCT

SEQ ID NO. 5204

STRAIN 18RS21

TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAAACAGATAAAA
 CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAATTGCC
 TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAC
 ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAAATGCGCTCCTTGATT
 TTGGACAATCCGCAGTAGAAGGCGTTAATACCACTGTTAATCATATCTTG
 TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
 TGCTAATCGCGAACTAAATGGATTATTTGCCAAATATAAAGATGCTACTC
 CGGCAGAATTAGAGAAAAAACCAAACTTGATTCAAAAATTATTCAAACAA
 AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
 AAAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAAGATACTTTGG
 CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATACTAAATCT
 ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
 GGTGCTAATCGTGCAAGCCACTTACAACAAGAAATTTCTAGCATTAGATA
 GCCAAACGTCCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT
 GAAATTATCAATACCCCTCGAACAGCAACATCCTGAATATGTCAGCCGTCT
 CTACGTTGCATGGGCAACAACACCACAGATGCGAAACTTGGTCAAAGTAT
 CGTCAGATATGCGTCAGAACTTGGCATGTTACGTCGAAATACCATTCCA
 ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
 ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
 AGATGCTGGCTGAAACTAGTAAGAAGCGATTCCGATGTTAGAGAAGACC
 GCACAAAGCCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
 CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
 AGGAACGTGCCaAATTGGGAATCTGCTGTTATTAAATCGGCTGAAACAATC
 AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
 CGAAGGTaAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5205

STRAIN M732

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC
 AATGCTATCACTAAAAACAGATAAAAAACAACAGAAATTATTTCCAACCAGAC
 AACAGCCAAACTGGGCAAATTGCCTTTTTGAAAACTAACACCAGCAC
 AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTCT
 GGTGACCAAAATGCGCTCCTTGATTTTTGACAATCCGCAGTAGAAGGCGT
 TAATACTACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC
 CTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTT
 ATTGCCAAATATAAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAA
 CTTGATTCAAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
 ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAT
 GTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT
 GCTCATTGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATTG
 CTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
 CAACAAGAAATTTCTAGCAATTAGATAGCCAAACGTCGGAATATCAAATTAA
 AAGTAACCAATTAGCCCCGAATGACTGAAGTTATCAATACCCCTCGAACAGC
 AACATACGGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA
 CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAAACTTGG
 TATGTTACGTCGAAATACCAATTCACAACATGAAACTCTCAATCGCTCAGT
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
 GTCAACGCTAATAATGCGAGCATTTGCAAAATGCTGGCTGAAACTAGTAAGA
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
 AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
 ATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAACTCTGC
 TGTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA
 G

SEQ ID NO. 5206

STRAIN COH1

CTAAAACAGATAAAAAACAACAGAAATTATTTCCAACCAGACAACAAGCCAA
 ACTGGGCAAATTGCCTTTTTTGAAAACTAACACCAGCACAAAAGTCTGC
 TwTCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTGGTGACCAAA
 ATGCGCTCCTTGATTTTTGACAATCCGCAGTAGAAGGCGTTAATACTACT
 GTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGA
 TGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTTATTGCCAAAT
 ATAAAGATGCTACTCCGGCaGAATTAGAGAAAAAACCAACTTGATTCAA
 AAATTATTCAAACAAGCAAGACCTCGCTACAGGAATTTTATTTTGACTC
 ACAAACATCGAGCAAAAAATGGATATGATGGCAGCAAATGTTGTCAAAC
 AAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAATGCTCATTGAA
 GATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGA
 ATCGAGTCAAGCCGAgGCTGCCAATCGTGCaAGCCACTTACAACAaGAAA
 TTCTAGCaTTAGATAGCCAAACGTCGGAATATCAAATTAAGTAACCAA
 TTAGCCCCGAATGACTGAaGTTATCAaTaCCCTCGAACAGCAACATACGGA
 aTATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCACAGATGCGAA
 ACTTGGTCAAAGTATCGTCAGATATGCGTCAGAAACTTGGTATGTTACGT
 CGAAATACCATTCCAACAATGAAACTCTCAATCGCTCAGTTAGGCATGAT
 GCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATTGTCAACGCTA
 ATAATGCAGCATTGCAAATGCTGGCTGAACTAGTAAGAAGCGATTCCG
 ATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTAAATCTGTAC

Table 52: Comparative Sequences relating to SAG 1823

TGCATTAGCTGAAAGCTTAGTGGCTCAAATAATGGTATTATCGCTGCCA
TAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGCTGTTATTAAA
TCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATAAAAAATAGT
TGAAGCCTTACTCAaCGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGT
CT

SEQ ID NO. 5207

STRAIN M781

TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAACAGATAAAA
CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAATTGCC
TTTTTTGAAAAAATAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGTGACCAAATGCGCTCCTTGATT
TTGGACAATCCGCAGTAGAAGGCGTTAATACTACTGTATCATATCTTG
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
CGGCAGAATTAGAGAAAAAACCAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCAAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCCAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGTCCGAATATCAAATTAAGTAACCAATTAGCCGAATGACT
GAAGTTATCAATACCCTCGAACAGCAACATACGGAATATGTGAGCCGTCT
CTACGTTGCATGGGCAACAACACCACAGATGCGAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAACTTGGTATGTTACGTCGAAATACCATTCCA
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AAATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAACGTGCCCAATTAGAATCTGCTGTTATTAAATCGGCTGAAACAATC
AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5208

STRAIN CJB110

TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAACAGATAAAA
CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAATTGCC
TTTTTTGAAAAAATAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAATGCGCTCCTTGATT
TTGGACAATCCGCAGTAGAAGGCGTTAATACTACTGTATCATATCTTG
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
CGGCAGAATTAGAGAAAAAACCAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGTCCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT
GAAGTTATCAATACCCTCGAACAGCAaCATACTGAATATGTGAGCCGTCT
CTACGTTGCATGGGCaAcAACACCACAGATGCGAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAACTTGGCATGTTACGTCGAAATACCATTCCA
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AGATGCTGGCTgAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAaCGTGCCCAATTGGAATCTGCTGTTATTAAATCGGCTGAAACAATC
AATGATTCTGTCAAAATTCGTGATaAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5209

STRAIN 1169NT

GCAGACAATGCTATCACTAAAACAGATAAAAACAGAAATTATTTCCAA
CCAGACAACAAGCCAAACTGGGCAAATTGCCCTTTTGTGAAAAAATAACAC
CAGCACAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACT
TTTGTGGTGACCAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGA
AGGCGTTAATACCAGTCTTAATCATATCTTGTCTGAGCAGAAAAAATTC
AAATTCCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAAT
GGATTTATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAA
ACCAAACTTGATCCAAAAATTATTCAAACAAGCAAGACCTCACTACAGG
AATTTTATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCA
GCAAAATGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGC
TGAAATGCTCATTGAAGATAATACTAAATCTATTGAAAAATTTGGTTGGAG
TTATTGCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGC
CACTTACAACAAGAAATTCAGCATTAGATAGCCAAACGTCCGAGTATCA
AATTAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCG
AaCAGCAACATACTGAATATGTGAGCCGTCTCTACGTTGCATGGGCAACA
aCACCACAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAA
ACTTGGCATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCG
CTCAGTTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGAT
GCTATTGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAG

Table 52: Comparative Sequences relating to SAG 1823

TAAAGAAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTT
 CTATTAAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAAT
 GGTATTATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGA
 ATCTGCTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTC
 GTGATAAAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAA
 GAAAAAGTTGATGAGTCT

SEQ ID NO. 5210

STRAIN JM9130013

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC
 AATGCTATCACTAAAAACAGATAAAAAACAGAAATTATTTCCAACCAGAC
 AACAGCCAAACTGGGCAAATTGCCTTTTTTGA AAAACTAACACCAGCAC
 AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTC
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 TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC
 CTCAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTT
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 CTTTATTTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
 CAACAAGAAATTTAGCATTAGATAGCCAAACGTCCGAGTATCAAATtAA
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 CATGTTACGTCGAAATACCATTTCCAACAATGAAACTCTCAATCGCTCAGT
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
 GTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAGA
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
 AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
 ATCGCTGCCATAGACAAAGGaCGTAAGGAACGTGCCCAATTAGAATCTGC
 TGTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAAGAAAA
 GTTGTGATGAGTCT

SEQ ID NO. 5211

STRAIN 2603

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 t

PRETTY of: /biotmp/msa13607.2{*} April 22, 2002 03:55 ..

	1				50
msa13607.2{201_COH1}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~C
msa13607.2{201_M781}	~~~~~	~~~~~TTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_090}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_CJB110}	~~~~~	~~~~~TTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_18RS21}	~~~~~	~~~~~TTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_2603}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_A909}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_H36B}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_JM9130013}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_1169NT}	~~~~~	~~~~~	~~~~~	~~~~~GCAGACA	ATGCTATCAC
msa13607.2{201_M732}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
Consensus	*****	*****	*****	*****	*****

Table 52: Comparative Sequences relating to SAG 1823

	51		100
msa13607.2{201_COH1}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_M781}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_090}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_CJB110}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_18RS21}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_2603}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_A909}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_H36B}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_JM9130013}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_1169NT}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_M732}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC CAACCAGACA ACAaGCCAAA
Consensus	*****	*****	*****
	101		150
msa13607.2{201_COH1}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_M781}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_090}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_CJB110}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_18RS21}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_2603}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_A909}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_H36B}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_JM9130013}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_1169NT}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_M732}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA CACCAGCACA AAAGTCTGCT
Consensus	*****	*****	*****
	151		200
msa13607.2{201_COH1}	WTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
msa13607.2{201_M781}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
msa13607.2{201_090}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GcGAtCAAAA
msa13607.2{201_CJB110}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GcGAtCAAAA
msa13607.2{201_18RS21}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GcGAtCAAAA
msa13607.2{201_2603}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GcGAtCAAAA
msa13607.2{201_A909}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
msa13607.2{201_H36B}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
msa13607.2{201_JM9130013}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
msa13607.2{201_1169NT}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
msa13607.2{201_M732}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT ACTTTTGTCTG GtGAcCAAAA
Consensus	-*****	*****	*****
	201		250
msa13607.2{201_COH1}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACTACTG
msa13607.2{201_M781}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACTACTG
msa13607.2{201_090}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_CJB110}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_18RS21}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_2603}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_A909}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_H36B}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_JM9130013}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_1169NT}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_M732}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT AGAAGGCGTT AATACTACTG
Consensus	*****	*****	*****
	251		300
msa13607.2{201_COH1}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_M781}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_090}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_CJB110}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_18RS21}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_2603}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_A909}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_H36B}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_JM9130013}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_1169NT}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_M732}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
Consensus	*****	*****	*****
	301		350
msa13607.2{201_COH1}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA AATGGATTTA TTGCCAAATA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M781}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_090}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_CJB110}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_18RS21}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_2603}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_A909}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_H36B}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_JM9130013}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_1169NT}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_M732}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
Consensus	*****	*****	*****	*****	*****
	351				400
msa13607.2{201_COH1}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M781}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_090}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_CJB110}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_18RS21}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_2603}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_A909}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_H36B}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_JM9130013}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_1169NT}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M732}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
Consensus	*****	*****	*****	*****	*****-*****
	401				450
msa13607.2{201_COH1}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M781}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_090}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_CJB110}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_18RS21}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_2603}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_A909}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_H36B}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_JM9130013}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_1169NT}	AATTATTCAA	ACAAAGCAAG	ACCTCaCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M732}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
Consensus	*****	*****	*****-*****	*****	*****
	451				500
msa13607.2{201_COH1}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M781}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_090}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_CJB110}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_18RS21}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_2603}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_A909}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_H36B}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_JM9130013}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCgAATG	TTGTCAAACA
msa13607.2{201_1169NT}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M732}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
Consensus	*****	*****	*****	*****-*****	*****
	501				550
msa13607.2{201_COH1}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M781}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_090}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_CJB110}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_18RS21}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_2603}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_A909}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_H36B}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_JM9130013}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_1169NT}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M732}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa13607.2{201_COH1}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M781}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_090}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_CJB110}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_18RS21}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_2603}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_A909}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAwTGC	TTTTATTGAA
msa13607.2{201_H36B}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_JM9130013}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_1169NT}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M732}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
Consensus	*****	*****	*****	*****-***	*****
601					
msa13607.2{201_COH1}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M781}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_090}	TCGAGTCAAG	CCGAGGCTGC	tAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_CJB110}	TCGAGTCAAG	CCGAGGCTGC	tAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_18RS21}	TCGAGTCAAG	CCGAGGCTGC	tAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_2603}	TCGAGTCAAG	CCGAGGCTGC	tAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_A909}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_H36B}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_JM9130013}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_1169NT}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M732}	TCGAGTCAAG	CCGAGGCTGC	cAATCGTGCA	AGCCACTTAC	AACAAGAAAT
Consensus	*****	*****	-*****	*****	*****
651					
msa13607.2{201_COH1}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_M781}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_090}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_CJB110}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_18RS21}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_2603}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_A909}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_H36B}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_JM9130013}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_1169NT}	TCTAGCATTa	GATAGCCAAA	CGTCCGAgtTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_M732}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
Consensus	*****	*****	*****-*	*****	*****
701					
msa13607.2{201_COH1}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_M781}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_090}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_CJB110}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_18RS21}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_2603}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_A909}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_H36B}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_JM9130013}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_1169NT}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_M732}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
Consensus	****-*****	*****	*****	*****	*****-*-****
751					
msa13607.2{201_COH1}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M781}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_090}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_CJB110}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_18RS21}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_2603}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_A909}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_H36B}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_JM9130013}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_1169NT}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M732}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
Consensus	*****	*****	*****	*****	*****
801					
msa13607.2{201_COH1}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_M781}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_090}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_CJB110}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_18RS21}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_2603}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_A909}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_H36B}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC
msa13607.2{201_JM9130013}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC
msa13607.2{201_1169NT}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC
msa13607.2{201_M732}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
Consensus	*****	*****	*****	-*****-	*****
851					
msa13607.2{201_COH1}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M781}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_090}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_CJB110}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_18RS21}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_2603}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_A909}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_H36B}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_JM9130013}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_1169NT}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M732}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
Consensus	*****	*****	*****	*****	*****
901					
msa13607.2{201_COH1}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M781}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_090}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_CJB110}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_18RS21}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_2603}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_A909}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_H36B}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_JM9130013}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_1169NT}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M732}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
Consensus	*****	*****	*****	*****	*****
951					
msa13607.2{201_COH1}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M781}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_090}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_CJB110}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_18RS21}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_2603}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_A909}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_H36B}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_JM9130013}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_1169NT}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M732}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
Consensus	*****	*****-****	*****	*****	*****
1001					
msa13607.2{201_COH1}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M781}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_090}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_CJB110}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_18RS21}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_2603}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_A909}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_H36B}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_JM9130013}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_1169NT}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M732}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
Consensus	*****	*****	*****	*****	*****
1051					
msa13607.2{201_COH1}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_M781}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_090}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_CJB110}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_18RS21}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_2603}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_A909}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_H36B}	GCATTAtCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_JM9130013}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_1169NT}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****	*****	*****	*****	*****
1100					
msa13607.2{201_COH1}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_M781}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_090}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_CJB110}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_18RS21}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_2603}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_A909}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_H36B}	GCATTAtCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_JM9130013}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_1169NT}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****	*****	*****	*****	*****

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M732}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****-***	*****	*****	*****	*****
	1101				1150
msa13607.2{201_COH1}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M781}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_090}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_CJB110}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_18RS21}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_2603}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_A909}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_H36B}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_JM9130013}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_1169NT}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M732}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
Consensus	*****	*****-****	*****	-*****	*****
	1151				1200
msa13607.2{201_COH1}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M781}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_090}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_CJB110}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_18RS21}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_2603}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_A909}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_H36B}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_JM9130013}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_1169NT}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M732}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa13607.2{201_COH1}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M781}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_090}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_CJB110}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_18RS21}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_2603}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_A909}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_H36B}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_JM9130013}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_1169NT}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M732}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	-----
Consensus	*****	*****	*****	*****	-----
	1251				
msa13607.2{201_COH1}	t				
msa13607.2{201_M781}	t				
msa13607.2{201_090}	t				
msa13607.2{201_CJB110}	t				
msa13607.2{201_18RS21}	t				
msa13607.2{201_2603}	t				
msa13607.2{201_A909}	t				
msa13607.2{201_H36B}	t				
msa13607.2{201_JM9130013}	t				
msa13607.2{201_1169NT}	t				
msa13607.2{201_M732}	-				
Consensus	-				

SEQ ID NO. 5212

STRAIN_090 frame: 1

SDTFNFDIDQIADNAITKTDKTTTEIISNQTTSTGTGQIAFFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSFYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESQSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 52013

STRAIN A909 frame: 1

SDTFNFDIDQIADNAITKTDKTTTEIISNQTTSTGTGQIAFFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM

Table 52: Comparative Sequences relating to SAG 1823

LIEDNTKSIENLVGVXAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5214

STRAIN H36B frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5215

STRAIN 18RS21 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTTPAQKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDN
TKSIENLVGVIAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHPEYVSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESAAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5216

STRAIN M732 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEK

SEQ ID NO. 5217

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFFEKLTTPAQKSAXSEKTPALVDTFVGDQNALLDGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIA
FIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ
LESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5218

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFFEKLTTPAQKSAXSEKTPALVDTFVGDQNALLDGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIA
FIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ
LESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5219

STRAIN M781 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTTPAQKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDN
TKSIENLVGVIAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESAAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5220

STRAIN CJB110 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTTPAQKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDN
TKSIENLVGVIAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESAAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5221

STRAIN 1169NT frame: 1

ADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTTPAQKSAISEKTPALVDTFVGDQNALLD
FGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNL
IQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIEN
LVGVIAFIESSQAEAAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEY
VSRLYVAVATTTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTAD
AIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGR

Table 52: Comparative Sequences relating to SAG 1823

KERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5222

STRAIN JM9130013 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFFEKLTPAQKSAISEKTPALVD
 TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIKAKYKDA
 TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIQKMDMMAANVVKQEDTLARNIVSAEM
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
 INTLEQQHPEYVSRLYVAVATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
 QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
 NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5223

STRAIN 2603 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFFEKLTPAQKSAISEKTPALVD
 TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIKAKYKDA
 TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIQKMDMMAANVVKQEDTLARNIVSAEM
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
 INTLEQQHPEYVSRLYVAVATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
 QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
 NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

PRETTY of: /biotmp/msa28369.2{*} April 22, 2002 04:27 ..

	1				50
msa28369.2{201_090}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_1169NT}	-----	-adnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_A909}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_JM9130013}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_COH1}	-----	-----KTD	KTTEIISNQT	TcQTGQIAFF	EKLTPAQKSA
msa28369.2{201_CJB110}	-----	fdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF
msa28369.2{201_M781}	-----	fdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF
msa28369.2{201_2603}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_H36B}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_18RS21}	-----	fdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF
msa28369.2{201_M732}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
Consensus	-----	-----	*****	*-*****	*****
	51				100
msa28369.2{201_090}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_1169NT}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_A909}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_JM9130013}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_COH1}	xSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_CJB110}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M781}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_2603}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_H36B}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_18RS21}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M732}	iSEKTPALVD	TFVGDQNALL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
Consensus	-*****	*****	*****	*****	*****
	101				150
msa28369.2{201_090}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_1169NT}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_A909}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_JM9130013}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_COH1}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_CJB110}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_M781}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_2603}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_H36B}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_18RS21}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
msa28369.2{201_M732}	DLLKNANREL	NGFIKAKYKDA	TPAELEKKPN	LIQKLFKQSK	TSLQEFYFDS
Consensus	*****	*****	*****	*****	*****
	151				200
msa28369.2{201_090}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_1169NT}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_A909}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVxAFIE
msa28369.2{201_JM9130013}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_COH1}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_CJB110}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M781}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_2603}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_H36B}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE

Table 52: Comparative Sequences relating to SAG 1823

msa28369.2{201_18RS21}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M732}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
Consensus	*****	*****	*****	*****	*****
	201				250
msa28369.2{201_090}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_1169NT}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_A909}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_JM9130013}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_COH1}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_CJB110}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M781}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_2603}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_H36B}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_18RS21}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M732}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
Consensus	*****	*****	*****	*****	*****
	251				300
msa28369.2{201_090}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_1169NT}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_A909}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_JM9130013}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_COH1}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_CJB110}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_M781}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_2603}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_H36B}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_18RS21}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
msa28369.2{201_M732}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSIAQLGMM
Consensus	*****	*****	*****	*****	*****
	301				350
msa28369.2{201_090}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_1169NT}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_A909}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_JM9130013}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_COH1}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_CJB110}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M781}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_2603}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_H36B}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_18RS21}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M732}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
Consensus	*****	*****	*****	*****	*****
	351				400
msa28369.2{201_090}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_1169NT}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_A909}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_JM9130013}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_COH1}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_CJB110}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M781}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_2603}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_H36B}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_18RS21}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M732}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
Consensus	**~*****	*****	*****	*****	*****
	401		417		
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	*****			

Table 53: Comparative Sequences relating to SAG 0755**SEQ ID NO. 5301****STRAIN 2603**

acaaatactttgaaaaaagaatttagttgaagctaaaaagacaattccatc
 cgtaaaagcttcaaaagtaccgcaaaaatcaacatcatcgaaagataaag
 agtttgttcttaaaaccgattatcgatgtctctgggtggcaacttccaaag
 gagattgattacgatacgttttcaaaaaatatttcaggtgttgattatcg
 tgtctttgggtggatcaaagatatctaagactaataacgctgcttatacaa
 ctggaatcgataaatcgtttaagacccatatacaagaatttcaaaagcga
 aatatcccagtagctgtctacagttatgcacttggttcaagtggttaaaga
 aatgaaagaagaggctcagatatatttataagaatgcagctccttacaac
 caactttttatttgattgacgtagaagaggagacaatgtctaactgaat
 aaaggtgtccaagcattccgaaaaagaattaaaaagacttggtgctaaaaa
 tgttggtatctacatttggtacttactttatgactgagcaaggcatctctg
 taaaaggatttgacgctgtttggattccaacttatggtagcgattctgga
 tactatgaagcggctccgcaactgaacttaaatacgatttacaccaata
 cacctctcaaggttatctaccaggawtcaatcaaccgcttgattttaatc
 aattgacagttaataaagacaagaagaaaacttatgagaaactttttgga
 aaagtaaaagag

SEQ ID NO. 5302**STRAIN 090**

ACAAATACTTTGAAAAAGAATTAG
 TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAA
 AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
 TGTCTCTGGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTCAA
 AAAATATTTTCAAGGTGTTGTTATTTCGTGTCTTTGGTGGATCAAAGATATCT
 AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGAC
 CCATATCAAAGAATTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTT
 ATGCACCTTGGTTCAAGTGTTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
 TATAAGAATGCAGCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGA
 AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCGAAAAG
 AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
 TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGAT
 TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG
 AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
 TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
 GAAAACCTTATGAGAACTTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5303**STRAIN A909**

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAA
 AGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATCA
 TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG
 GCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAATATTTTCA
 GTGTTGTTATTTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
 GCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGA
 ATTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTTTATGCACCTTGGTT
 CAAGTGTTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCA
 GCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGAAGAGGAGACAAT
 GTCTAACATGAATAAAGGTGTCCAAGCATTCGAAAAGAAATTAAAAAGAC
 TTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAG
 CAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACCTTATGG
 TAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACG
 ATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
 CTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATGA
 GAACTTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5304**STRAIN H36B**

ACAAATACTTTGAAAAAGAATTAG
 TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAA
 AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
 TGTCTCTGGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
 AAAATATTTTCAAGGTGTTGTTATTTCGTGTCTTTGGTGGATCAAAGATATCT
 AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGAC
 CCATATCAAAGAATTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTT
 ATGCACCTTGGTTCAAGTGTTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
 TATAAGAATGCAGCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGA
 AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCGAAAAG
 AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
 TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGAT
 TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG
 AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
 TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
 GAAAACCTTATGAGAACTTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5305**STRAIN 18RS21**

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAA
 GACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATCAT
 CGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGG
 CAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAATATTTTCAAG
 TGTGTTATTTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACG

Table 53: Comparative Sequences relating to SAG 0755

CTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGAA
 TTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGTTC
 AAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCAG
 CTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAATG
 TCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAAGAATTAAAAAGACT
 TGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAGC
 AAGGCATCTCTGTAAAAGGATTTGACGCTGTTGGATTCCAACCTATGGT
 AGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACGA
 TTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGC
 TTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATGAG
 AAACTTTTTGAAAAAGTAAAAGAG

SEQ ID NO. 5306

STRAIN M732

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA
 AAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT
 GGCAACTTCTAAGGAGATTGATTACGATACGCTTCAA AAAAATATTTCA
 GGTGTTGTTATTTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG
 AATTTCAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGT
 TCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGC
 AGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAAGAGTTAAAAAGA
 CTTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
 GCAAGGTATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACCTATG
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
 GCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATG
 AGAAACTTTTTTGAAAAAGTAAAAGAG

SEQ ID NO. 5307

STRAIN COH1

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA
 AGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
 TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG
 GCAACTTCTAAGGAGATTGATTACGATACGCTTCAA AAAAATATTTCA
 GTGTTGTTATTTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
 GCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGA
 ATTTCAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGT
 CAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCA
 GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT
 GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAAGAGTTAAAAAGAC
 TTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAG
 CAAGGTATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACCTATGG
 TAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATACG
 ATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
 CTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATGA
 GAAACTTTTTTGAAAAAGTAAAAGAG

SEQ ID NO. 5308

STRAIN M781

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA
 AAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT
 GGCAACTTCTAAGGAGATTGATTACGATACGCTTCAA AAAAATATTTCA
 GGTGTTGTTATTTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG
 AATTTCAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGT
 TCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGC
 AGCTCCTTACAAACCAACTTTTTatTGGATTGACGTAGAAGAGGAGaCAA
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAAGAGTTAAAAAGA
 CTTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
 GCAAGGTATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACCTATG
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
 GCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATG
 AGAAACTTTTTTGAAAAAGTAAAAGAG

SEQ ID NO. 5309

STRAIN CJB110

AAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCCATCCG
 TAAAAGCTTCAAAGTACCGCAAAAATCAACATCATCGAAAGATAAAGAG
 TTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCTAAGGA
 GATTGATTACGATACGCTTTCAA AAAAATATTTCAAGGTGTTGTTATTCTG
 TCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATACAACT
 GGAATCGATAAATCGTTTAAAGACCCATATCAAAGAATTTCAAAGCGAAA
 TATCCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTTAAAGAAA
 TGAAAGAAGAGGCTCAGATATTTTATAAGAATGCAGCTCCTTACAAACCA
 ACTTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATGAATAA
 AGGTGTCCAAGCATTCCGAAAAAGAATTAAAAAGACTTGGTGCTAAAAATG
 TTGGTATCTACATTGGTACTTACTTTATGACTGAGCAAGGCATCTCTGTA
 AAAGGATTTGACGCTGTTTGGATTCCAACCTATGGTAGCGATTCTGGATA

Table 53: Comparative Sequences relating to SAG 0755

CTATGAAGCGGCTCCGCAAACTGAACCTTAAATACGATTTACACCAATACA
CCTCTCAAGGTTATCTACCAGGATTCATCAACCGCTTGATTTAAATCAA
ATTACAGTTAATAAAGACAAGAAGAAAACCTTATGAGAACTTTTGGAAA
AGTAAAAGAG

SEQ ID NO. 5310

STRAIN 1169NT

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCC
ATCCGTAAAAGCTTCAAAAGTACCGCAAAATCAACATCATCGAAAGATA
AAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCCT
AAGGAGATTGATTACGATACGCTTTCAAAAAATATTTAGGTGTTGTTAT
TCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATA
CAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGAATTTCAAAG
CGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTTAA
AGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCAGCTCCTTACA
AACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATG
AATAAAGGTGTCCAAGCATTCGAAAAGAATTAAAAAGACTTGGCGCTAA
AAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAGCAAGGTATCT
CTGTAAAAGGATTTGACGCTGTTTGGATTCCAACCTTATGGTAGCGATTCT
GGATACTATGAAGCAGCTCCGCAAACTGAACCTTAAATACGATTTACACCA
ATACACCTCTCAAGGTTATCTACCAGGATTCATCAACCGCTTGATTTAA
ATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATGAGAACTTTT
GGAAAAGTAAAAGAG

SEQ ID NO. 5311

STRAIN JM9130013

ACAAATACTTTGAAAAAGAATTAG
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTTCAAGGTGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGAC
CCATATCAAAGAATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTT
ATGCACTTGGTTCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGAT
TCCAACCTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

PRETTY of: /biotmp/msa21441.2{*} January 20, 2003 03:46 ...

	1				50
msa21441.2{206_090}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_18RS21}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_2603}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_A909}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_H36B}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_JM9130013}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_CJB110}	--AAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_COH1}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_M732}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_M781}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_1169NT}	acAAATACTT	TGAAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
Consensus	--*****	*****	*****	*****	*****
	51				100
msa21441.2{206_090}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_18RS21}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_2603}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_A909}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_H36B}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_JM9130013}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_CJB110}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_COH1}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M732}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M781}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_1169NT}	CGTAAAAGCT	TCAAAAGTAC	CGCAAAAATC	AACATCATCG	AAAGATAAAG
Consensus	*****	*****	*****	*****	*****
	101				150
msa21441.2{206_090}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_18RS21}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_2603}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_A909}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_H36B}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_JM9130013}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_CJB110}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_COH1}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_M732}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M781}	AGTTTGTTC	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_1169NT}	AGTTTGTTC	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_18RS21}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_2603}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_A909}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_H36B}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_JM9130013}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_CJB110}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_COH1}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_M732}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_M781}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_1169NT}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_18RS21}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_2603}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_A909}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_H36B}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_JM9130013}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_CJB110}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_COH1}	TaTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_M732}	TaTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_M781}	TaTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_1169NT}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
Consensus	*-*****	*****	*****	*****	*****
msa21441.2{206_090}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_18RS21}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_2603}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_A909}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_H36B}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_JM9130013}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_CJB110}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_COH1}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_M732}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_M781}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
msa21441.2{206_1169NT}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAGCGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_18RS21}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_2603}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_A909}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_H36B}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_JM9130013}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_CJB110}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_COH1}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_M732}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_M781}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_1169NT}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_18RS21}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_2603}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_A909}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_H36B}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_JM9130013}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_CJB110}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_COH1}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_M732}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_M781}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_1169NT}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_18RS21}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_2603}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_A909}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_H36B}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_JM9130013}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_CJB110}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_COH1}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M732}	CAACTTTT	TTGGATTG	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_M781}	CAACTTTT	TTGGATTG	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_1169NT}	CAACTTTT	TTGGATTG	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
Consensus	*****	*****	*****	*****	*****
451					
msa21441.2{206_090}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_18RS21}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_2603}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_A909}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_H36B}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_JM9130013}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_CJB110}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_COH1}	AAAGGTGTCC	AAGCATTCCG	AAAAGAgTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M732}	AAAGGTGTCC	AAGCATTCCG	AAAAGAgTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M781}	AAAGGTGTCC	AAGCATTCCG	AAAAGAgTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_1169NT}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GcGCTAAAAA
Consensus	*****	*****	*****-***	*****	*-*****
501					
msa21441.2{206_090}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_18RS21}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_2603}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_A909}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_H36B}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_JM9130013}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_CJB110}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_COH1}	TGTTGGTATC	TACATcGGTA	CTTACTTTAT	GACTGAGCAA	GGtATCTCTG
msa21441.2{206_M732}	TGTTGGTATC	TACATcGGTA	CTTACTTTAT	GACTGAGCAA	GGtATCTCTG
msa21441.2{206_M781}	TGTTGGTATC	TACATcGGTA	CTTACTTTAT	GACTGAGCAA	GGtATCTCTG
msa21441.2{206_1169NT}	TGTTGGTATC	TACATcGGTA	CTTACTTTAT	GACTGAGCAA	GGtATCTCTG
Consensus	*****	*****-***	*****	*****	**-*****
551					
msa21441.2{206_090}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_18RS21}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_2603}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_A909}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_H36B}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_JM9130013}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_CJB110}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_COH1}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M732}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M781}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_1169NT}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
Consensus	*****	*****	*****	*****	*****
601					
msa21441.2{206_090}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_18RS21}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_2603}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_A909}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_H36B}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_JM9130013}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_CJB110}	TACTATGAAG	CgGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_COH1}	TACTATGAAG	CaGCTCCaCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_M732}	TACTATGAAG	CaGCTCCaCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_M781}	TACTATGAAG	CaGCTCCaCA	AACTGAACTT	AAATACGATT	TACACCAATA
msa21441.2{206_1169NT}	TACTATGAAG	CaGCTCCgCA	AACTGAACTT	AAATACGATT	TACACCAATA
Consensus	*****	*-*****-*	*****	*****	*****
651					
msa21441.2{206_090}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_18RS21}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_2603}	CACCTCTCAA	GGTTATCTAC	CAGGawTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_A909}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_H36B}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_JM9130013}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_CJB110}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_COH1}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_M732}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_M781}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_1169NT}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
Consensus	*****	*****	*****-***	*****	*****
701					
msa21441.2{206_090}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_18RS21}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_2603}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_A909}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_H36B}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_JM9130013}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_CJB110}	AAATTaCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_COH1}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
msa21441.2{206_M732}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
msa21441.2{206_M781}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
msa21441.2{206_1169NT}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
Consensus	*****-***** ***** ***** ***** ***** *****
	751 762
msa21441.2{206_090}	AAAGTAAAAG AG
msa21441.2{206_18RS21}	AAAGTAAAAG AG
msa21441.2{206_2603}	AAAGTAAAAG AG
msa21441.2{206_A909}	AAAGTAAAAG AG
msa21441.2{206_H36B}	AAAGTAAAAG AG
msa21441.2{206_JM9130013}	AAAGTAAAAG AG
msa21441.2{206_CJB110}	AAAGTAAAAG AG
msa21441.2{206_COH1}	AAAGTAAAAG AG
msa21441.2{206_M732}	AAAGTAAAAG AG
msa21441.2{206_M781}	AAAGTAAAAG AG
msa21441.2{206_1169NT}	AAAGTAAAAG AG
Consensus	***** **

SEQ ID NO. 5312

STRAIN 2603 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGXNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5313

STRAIN 090 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5314

STRAIN A909 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5315

STRAIN H36B frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5316

STRAIN 18RS21 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5317

STRAIN M732 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRIFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5318

STRAIN COH1 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRIFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5319

STRAIN M781 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRIFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5320

STRAIN CJB110 frame: 2

NTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKNI
SGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSSVKEMKEE
AQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQG
ISVKGFDVWIPYTGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQTITVKNKDK
KKTYEKLFGKVKE

SEQ ID NO. 5321

STRAIN 1169NT frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVWIPYTGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQTITVKNKDK
KKTYEKLFGKVKE

SEQ ID NO. 5322

STRAIN JM9130013 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNI PAVVYSYALGSSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVWIPYTGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQTITVKNKDK
KKTYEKLFGKVKE

PRETTY of: /biotmp/msa21641.2{*} January 20, 2003 03:59 ..

	1				50
msa21641.2{206_090}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_1169NT}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_18RS21}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_2603}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_A909}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_H36B}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_JM9130013}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_COH1}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_M732}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_M781}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
msa21641.2{206_CJB110}	-NTLKKELVE	AKKTIPSVKA	SKVPQKSTSS	KDKEFVLKPI	IDVSGWQLPK
Consensus	*****	*****	*****	*****	*****
	51				100
msa21641.2{206_090}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_1169NT}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_18RS21}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_2603}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_A909}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_H36B}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_JM9130013}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_COH1}	EIDYDTLSKN	ISGVVIRiFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_M732}	EIDYDTLSKN	ISGVVIRiFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_M781}	EIDYDTLSKN	ISGVVIRiFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
msa21641.2{206_CJB110}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA	AYTTGIDKSF	KTHIKEFQKR
Consensus	*****	*****	*****	*****	*****
	101				150
msa21641.2{206_090}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_1169NT}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_18RS21}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_2603}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_A909}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_H36B}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_JM9130013}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_COH1}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_M732}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_M781}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
msa21641.2{206_CJB110}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA	PYKPTFYWID	VEEETMSNMN
Consensus	*****	*****	*****	*****	*****
	151				200
msa21641.2{206_090}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_1169NT}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_18RS21}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_2603}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_A909}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_H36B}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_JM9130013}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_COH1}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_M732}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_M781}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
msa21641.2{206_CJB110}	KGVAQAFRKEL	KRLGAKNVGI	YIGTYFMTEQ	GISVKGFDV	WIPTYGSDSG
Consensus	*****	*****	*****	*****	*****

Table 53: Comparative Sequences relating to SAG 0755

	201				250
msa21641.2{206_090}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_1169NT}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_18RS21}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_2603}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGxNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_A909}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_H36B}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_JM9130013}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_COH1}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_M732}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_M781}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_CJB110}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGfNQPL	DLNQItVNKD	KKKTYEKLFG
Consensus	*****	*****	*****	*****	*****
	251				
msa21641.2{206_090}	KVKE				
msa21641.2{206_1169NT}	KVKE				
msa21641.2{206_18RS21}	KVKE				
msa21641.2{206_2603}	KVKE				
msa21641.2{206_A909}	KVKE				
msa21641.2{206_H36B}	KVKE				
msa21641.2{206_JM9130013}	KVKE				
msa21641.2{206_COH1}	KVKE				
msa21641.2{206_M732}	KVKE				
msa21641.2{206_M781}	KVKE				
msa21641.2{206_CJB110}	KVKE				
Consensus	****				

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5401

STRAIN 2603

TTGACTCACAAAAATATATTATTAACCATTATATTTGGATTATTT
 ATGATTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATAATTGG
 GAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG
 GGATTTGAAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTIAGCTAATGCTGTT
 TTAAAGAATACGGTATTTTCACTGAAATGGCAGCCTATTAACGGGATATGAAAGAACT
 GAACCTTAATAATGGTAATATAGACCTTATTGGGAATGGTTATTCAAAAACGGCAGAACGT
 GCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAA
 ACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCGAGTCG
 GGTTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATATTTTAAAAAAGTTTGTAAAA
 GGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGCTTTGATTGATTAAAAAATAAC
 CGTATTGATGGTCTTTTGGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGA
 AATATAAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTTGTAGTAGGA
 GCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT
 AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGTTTATAGTAAA
 GAA

SEQ ID NO. 5402

STRAIN 090

ATTGGGaaCATTATC

AAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG
 GGATTTGAAAGCCGTTCTGGTGACTATACCGGCTTTGATATTGATTAGC
 TAATGCTGTTTTTAAAGAATACGGTATTTCACTGAAATGGCAGCCTATTA
 ACTGGGATATGAAAGAACTGAACCTAATAATGGTAATATAGACCTTATT
 TGGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC
 AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTTCATCAC
 ATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCGAGTCG
 GGTTTCATCTGGTTTTGATGCTTTTAATGCTAAACCTGATATTTTAAAAAA
 GTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGCTT
 TGATTGATTAAAAAATAACCGTATTGATGGTCTTTTGGATTGATGAAGTT
 TATGCTAACTATTATTAAAGCAAGAAGGAAATATAAAAGCTTATTATTT
 TGTTAAAACTGCTTATCAAGGAGAAAAATTTTGTAGTAGGAGCTCGCAAAG
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT
 AATAAGGGAAAATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
 TTATAGTAAAGAA

SEQ ID NO. 5403

STRAIN A909

ATTGGG

aACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTT
 GTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATAT
 TGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTGAAATGGC
 AGCCTATTAACTGGGATATgAAAGAACTGAACCTAATAATGGTAATATA
 GACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGT
 CGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAA
 CTTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGA
 GCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATAT
 TTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTCAATACGATACTTTCA
 CTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGGATT
 GATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATATAAAAGC
 TTATTATTTTGTAAAACTGCTTATCAAGGAGAAAATTTTGTAGTAGGAG
 CTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAA
 CAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGG
 TGAAGATGTTTATAGTAAAGaa

SEQ ID NO. 5404

STRAIN H36B

ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATT

TGATAATACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATA
 CCGGCTTTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATT
 TCAGTGAAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTAA
 TAATGGTAATATAGACCTTATTGGGAATGGTTATTCAAAAACGGCAGAAC
 GTGCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTA
 ATTGTTACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGG
 GAAAAAACTAGGAGCCCGAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACG
 CTAAACCTGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTCAA
 TACGATACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGA
 TGGTCTTTTGGATTGATGAAGTCTATGCTAACTATTATTAAAGCAAGAAG
 GAAATATAAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAaAAAAT
 TTTGTAGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAA
 CAAAGCTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTT
 ACAAAATGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5405

STRAIN 18RS21

ATTGGGAACATTA

TCAAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTA
 TGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTAA
 GCTAATGCTGTTTTTAAAGAATACGGTATTTCACTGAAATGGCAGCCTAT
 TAACTGGGATATGAAAGAACTGAACCTAATAATGGTAATATAGACCTTA
 TTTGGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTT
 ACAAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTTCATC

Table 54: Comparative Sequences relating to SAG0949

ACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGT
 CGGGTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATATTTTAAAA
 AAGTTTGTAAAAGGAAAAGAGCAGTTCAATACGATACTTTCACTCAGGC
 TTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATTGATGAAG
 TTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTAT
 TTTGTTAAAACTGCTTATCAAGGAGAAAAATTTTGTAGTAGGAGCTCGTAA
 AGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTC
 ATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGAT
 GTTTATAGTAAAGAA

SEQ ID NO. 5406

STRAIN M732

ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA
 TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
 TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAAGT
 AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTTAATAATGG
 TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTA
 AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
 ACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
 ACTAGGAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAAC
 CTGATATTTTAAAAAGTTTTGTAAAAGGAAAAGAGCAGTTCAATACGAT
 ACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCT
 TTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATA
 TAAAAGCTTATTATTTTGTAAAAGCTGCTTATCAAGGAGAAAAATTTGTA
 GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC
 TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT
 GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5407

STRAIN COH1

ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA
 TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
 TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAAGT
 AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTTAATAATGG
 TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTA
 AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
 ACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
 ACTAGGAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAAC
 CTGATATTTTAAAAAGTTTTGTAAAAGGAAAAGAGCAGTTCAATACGAT
 ACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCT
 TTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATA
 TAAAAGCTTATTATTTTGTAAAAGCTGCTTATCAAGGAGAAAAATTTGTA
 GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC
 TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT
 GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5408

STRAIN M781

ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA
 ATACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGC
 TTTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAAGT
 GAAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTTAATAATG
 GTAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCT
 AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGT
 TACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
 AACTAGGAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAA
 CCTGATATTTTAAAAAGTTTTGTAAAAGGAAAAGAGCAGTTCAATACGA
 TACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTC
 TTTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAAT
 ATAAAAGCTTATTATTTTGTAAAAGCTGCTTATCAAGGAGAAAAATTTGT
 AGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAG
 CTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAA
 TGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5409

STRAIN CJB110

ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA
 ACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTT
 TGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAAGTGA
 AATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTTAATAATGGT
 AATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAA
 AAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTA
 CTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
 CTAGGAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACC
 TGATATTTTAAAAAGTTTTGTAAAAGGAAAAGAGCAGTTCAATACGATA
 CTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTT
 TTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATAT
 AAAAGCTTATTATTTTGTAAAAGCTGCTTATCAAGGAGAAAAATTTGTAG
 TAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCT
 TTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATG
 GTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5410

Table 54: Comparative Sequences relating to SAG0949

STRAIN 1169NT

ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGAATATACCGGCT
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTTCACTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCAATAATGG
TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAACTTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
ACTAGGAGCCCGAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAATGCTAAAC
CTGACATTTTAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGAT
ACTTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCT
TTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTTTGTAAAAGTCTTATCAAGGAGAAAATTTTGTA
GTAGGAGCTCGCAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAAATTTCAAAAAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5411

STRAIN JM9130013

ATTGGGAACATTATC

AAAAGGAAAAGAAAATTACTATTGGATTGATAAATCTTTTGTTCCTATG
GGATTGAAAGTCGTTCTGGTGAATATACCGGCTTTGATATTGATTAGC
TAATGCTGTTTTTAAAGAATACGGTATTTTCACTGAAATGGCAGCCTATTA
ACTGGGATATGAAAGAACTGAACCTTAATAATGGTAATATAGACCTTATT
TGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGTTTTAC
AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTTCATCAC
ATATTAATAGTATTAAGGATATGAAGGGGAAAAAAGTAGGAGCCCGAGTCG
GGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATATTTTAAAAA
GTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGCTT
TGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATTGATGAAGTT
TATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAGCTTATTATTT
TGTTAAAAGTCTTATCAAGGAGAAAATTTGTAGTAGGAGCTCGTAAAG
TTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTCAT
AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
TTATAGTAAAGAA

PRETTY of: /biotmp/msa39314.2{*} February 18, 2003 11:01 ..

	1				50
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	ttgactcaca	aaaatatatt	attaaccatt	atatttggat	tatttatgat
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	tatattatca	gcatgtggtta	tgtctaataa	ggaaatggct	ggatttgata
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa39314.2{225_18RS21}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_2603}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_A909}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_CJB110}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_COH1}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_H36B}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_KM9130013}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_M732}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_M781}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_090}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
msa39314.2{225_1169NT}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTTGATAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa39314.2{225_18RS21}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGAAT	ATACCGGCTT
msa39314.2{225_2603}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGAAT	ATACCGGCTT

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_A909}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_CJB110}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_COH1}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_H36B}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_KM9130013}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_M732}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_M781}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_090}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_1169NT}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
Consensus	*****	*****	*****_***	*****	*****
msa39314.2{225_18RS21}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_2603}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_A909}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_CJB110}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_COH1}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_H36B}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_KM9130013}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_M732}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_M781}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_090}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
msa39314.2{225_1169NT}	TGATATTGAT	TTAGCTAATG	CTGTTTTTTAA	AGAATACGGT	ATTTTCAGTGA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_2603}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_A909}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_CJB110}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_COH1}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_H36B}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_KM9130013}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_M732}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_M781}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_090}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_1169NT}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	cAATAATGGT
Consensus	*****	*****	*****	*****	-*****
msa39314.2{225_18RS21}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_2603}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_A909}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_CJB110}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_COH1}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_H36B}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_KM9130013}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M732}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M781}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_090}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_1169NT}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_2603}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_A909}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_CJB110}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_COH1}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_H36B}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_KM9130013}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M732}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M781}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_090}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_1169NT}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_2603}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_A909}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_CJB110}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_COH1}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_H36B}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_KM9130013}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M732}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M781}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_090}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_1169NT}	CTAAAACCTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_2603}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_A909}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_CJB110}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_COH1}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_H36B}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_KM9130013}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M732}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M781}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_090}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AtGCTAAACC
msa39314.2{225_1169NT}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AtGCTAAACC
Consensus	*****	*****	*****	*****	*-*****
msa39314.2{225_18RS21}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_2603}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_A909}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_CJB110}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_COH1}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_H36B}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_KM9130013}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M732}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M781}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_090}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_1169NT}	TGAtATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
Consensus	***-*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_2603}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_A909}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_CJB110}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_COH1}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_H36B}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_KM9130013}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M732}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M781}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_090}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_1169NT}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_2603}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_A909}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_CJB110}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_COH1}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_H36B}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_KM9130013}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M732}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M781}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_090}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_1169NT}	TTGATTGATG	AAGTTTATGC	TAACTATTAT	TTAAAGCAAG	AAGGAAATAT
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_2603}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_A909}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_CJB110}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_COH1}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_H36B}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_KM9130013}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M732}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M781}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_090}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_1169NT}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_2603}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_A909}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_CJB110}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_COH1}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_H36B}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_KM9130013}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M732}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M781}	TAGGAGCTCG	tAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_090}	TAGGAGCTCG	cAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_1169NT}	TAGGAGCTCG	cAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
Consensus	*****	-*****	*****	*****	*****

751

800

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_18RS21}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_2603}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_A909}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_CJB110}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_COH1}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_H36B}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_KM9130013}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M732}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M781}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_090}	TTCAAACAGC	TTCATAATAA	GGGaAaATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_1169NT}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
Consensus	*****	*****	***-**-***	*****	*****

	801	828
msa39314.2{225_18RS21}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_2603}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_A909}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_CJB110}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_COH1}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_H36B}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_KM9130013}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M732}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M781}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_090}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_1169NT}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
Consensus	*****	*****

SEQ ID NO. 5412

STRAIN 2603 frame: 1

LTHKNILLTIIFGLFMIIISACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFVPMGFESR
SGDYGTFDIDLANAVFKEYGISVKWQPINWDMKETELNNGNIDLIWNGYSKTAERAKKVA
FTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQSGSSGFDAFNAKPDILKKFVKGKEAV
QYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEGNIKAYYFVKTAAYQGENFVVGARKVD
RRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYSKE

SEQ ID NO. 5413

STRAIN 090 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYGTFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEG
NIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5414

STRAIN A909 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYGTFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEG
NIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5415

STRAIN H36B frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYGTFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEG
NIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5416

STRAIN 18RS21 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYGTFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEG
NIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5417

STRAIN M732 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYGTFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEG
NIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5418

STRAIN COH1 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYGTFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEG
NIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5419

STRAIN M781 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKKLGAQ
 SGSSGFDNAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
 GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
 KE

SEQ ID NO. 5420

STRAIN CJB110 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKKLGAQ
 SGSSGFDNAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
 GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
 KE

SEQ ID NO. 5421

STRAIN 1169NT frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKKLGAQ
 SGSSGFDNAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
 GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
 KE

SEQ ID NO. 5422

STRAIN JM9130013 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKKLGAQ
 SGSSGFDNAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
 GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
 KE

PRETTY of: /biotmp/msa45901.2{*} February 19, 2003 03:09 ..

	1				50
msa45901.2{225_090}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_1169NT}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_18RS21}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_2603}	lthknillti	ifglfmiils	acgmsnkema	gidn	WEHYQK EKKITIGFDN
msa45901.2{225_A909}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_CJB110}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_COH1}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_H36B}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_JM9130013}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_M732}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_M781}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
Consensus	*****	*****	*****	*****	*****
	51				100
msa45901.2{225_090}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_1169NT}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_18RS21}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_2603}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_A909}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_CJB110}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_COH1}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_H36B}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_JM9130013}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M732}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M781}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
Consensus	*****	*****	*****	*****	*****
	101				150
msa45901.2{225_090}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_1169NT}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_18RS21}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_2603}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_A909}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_CJB110}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_COH1}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_H36B}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_JM9130013}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M732}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M781}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
Consensus	*****	*****	*****	*****	*****
	151				200
msa45901.2{225_090}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_1169NT}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_18RS21}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_2603}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_A909}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_CJB110}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL

Table 54: Comparative Sequences relating to SAG0949

msa45901.2{225_COH1}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_H36B}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_JM9130013}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M732}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M781}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
Consensus	*****	*****	*****	*****	*****
msa45901.2{225_090}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_1169NT}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_18RS21}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_2603}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_A909}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_CJB110}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_COH1}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_H36B}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_JM9130013}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M732}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M781}	LIDEVYANY	LKQEGNIKAY	YFVKTAYQGE	NFVVGARKVD	RRLIEKINKA
Consensus	*****	*****	*****	*****	*****
msa45901.2{225_090}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
Consensus	*****	*****	*****		

Table 55: Comparative Sequences relating to SAG1592

SEQ ID NO. 5501
STRAIN 2603
ATGCTTAAATCTTTTGTGATTTTCTTAGTTTCGCTTTTACCAAAAAATATTTCTCCAGCT
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTATTTTGGCATGTCATCCCTTA
GCCCCAGGAGGAAATGATCCTGTCCCTGATCATTTTAGCTTAAGACGTAATAAAACGGAT
ATATCAGAT

SEQ ID NO. 5502
STRAIN 090
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTT

SEQ ID NO. 5503
STRAIN A909
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATA

SEQ ID NO. 5504
STRAIN H36B
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5505
STRAIN 18RS21
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5506
STRAIN M732
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5507
STRAIN COH1
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTATTTTGGCATGTCATCCCTTA
GCCCCAGGAGGAAATGATCCTGTCCCTGATCATTTTAGCT

SEQ ID NO. 5508
STRAIN M781
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5509
STRAIN CJB110
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5510
STRAIN 1169NT
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
TATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5511
STRAIN JM9130013
TTCCCAGCTAGCTGTCTGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGGCATGTCATCCCTTAGCCCCAGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

PRETTY of: /biotmp/msa119306.2{*} April 29, 2003 06:23 ..

	1	50
msa119306.2{233_H36B}	-----	-----
msa119306.2{233_JM9130013}	-----	-----

Table 55: Comparative Sequences relating to SAG1592

msa119306.2{233_090}	-----	-----	-----	-----	-----
msa119306.2{233_18RS21}	-----	-----	-----	-----	-----
msa119306.2{233_2603}	atgctttaa	cttttttgat	tttcttagtt	cgctttttacc	aaaaaaatat
msa119306.2{233_A909}	-----	-----	-----	-----	-----
msa119306.2{233_CJB110}	-----	-----	-----	-----	-----
msa119306.2{233_COH1}	-----	-----	-----	-----	-----
msa119306.2{233_M732}	-----	-----	-----	-----	-----
msa119306.2{233_M781}	-----	-----	-----	-----	-----
msa119306.2{233_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					
msa119306.2{233_H36B}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_JM9130013}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_090}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_18RS21}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_2603}	ttctccagct	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_A909}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_CJB110}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_COH1}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_M732}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_M781}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
msa119306.2{233_1169NT}	-----	TTCCCAGCTA	GCTGTCGTTA	TCGTCCAACT	TGCTCTACGT
Consensus	*****	*****	*****	*****	*****
101					
msa119306.2{233_H36B}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctGATGGGG
msa119306.2{233_JM9130013}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctGATGGGG
msa119306.2{233_090}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_18RS21}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_2603}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_A909}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_CJB110}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_COH1}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M732}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M781}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_1169NT}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	ggTGATGGGG
Consensus	*****	*****	*****	*****	*****
151					
msa119306.2{233_H36B}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_JM9130013}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_090}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_18RS21}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_2603}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_A909}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_CJB110}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_COH1}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M732}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M781}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_1169NT}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
Consensus	*****	*****	*****	*****	*****
201					
msa119306.2{233_H36B}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_JM9130013}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_090}	TGTCCCTGAT	cATTTTAGCT	t-----	-----	-----
msa119306.2{233_18RS21}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_2603}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_A909}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	ata-----
msa119306.2{233_CJB110}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_COH1}	TGTCCCTGAT	cATTTTAGCT	-----	-----	-----
msa119306.2{233_M732}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_M781}	TGTCCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_1169NT}	TGTCCCTGAT	tATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
Consensus	*****	*****	-----	-----	-----

SEQ ID NO. 5512

STRAIN 2603 frame: 1

MLKSFLIFLVRFYQKNISPAFPASCYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPL
AHGNDPVPDHFSLRRNKTDISD

SEQ ID NO. 5513

STRAIN 090 frame: 1

FPASCYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGNDPVPDHF

SEQ ID NO. 5514

STRAIN A909 frame: 1

FPASCYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGNDPVPDHFSLRRNKTD
I

SEQ ID NO. 5515

STRAIN H36B frame: 1

Table 55: Comparative Sequences relating to SAG1592

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5516

STRAIN 18RS21 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5517

STRAIN M732 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5518

STRAIN COH1 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5519

STRAIN M781 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5520

STRAIN CJB110 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5521

STRAIN 1169NT frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDYFSLRRNKTD
ISD

SEQ ID NO. 5522

STRAIN JM9130013 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

PRETTY of: /biotmp/msa119415.2{*} April 29, 2003 06:25 ..

	1				50
msa119415.2{233_090}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_18RS21}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_COH1}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_A909}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_2603}	mlksfliflv	rffyqknispa	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_CJB110}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_H36B}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_JM9130013}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_M732}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_M781}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
msa119415.2{233_1169NT}	-----	-----	FPASCRYRPT	CSTYMIEAIQ	KHGLKGVLMG
Consensus	*****	*****	*****	*****	*****-*

	51				83
msa119415.2{233_090}	IARILRCHPL	AHGGNDPVPD	hFS-----	----	
msa119415.2{233_18RS21}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_COH1}	IARILRCHPL	AHGGNDPVPD	hFS-----	----	
msa119415.2{233_A909}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	I--	
msa119415.2{233_2603}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_CJB110}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_H36B}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_JM9130013}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_M732}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_M781}	IARILRCHPL	AHGGNDPVPD	hFSLRNKTD	ISD	
msa119415.2{233_1169NT}	IARILRCHPL	AHGGNDPVPD	yFSLRNKTD	ISD	
Consensus	*****	*****	-*****	***	

Table 56: Comparative Sequences relating to SAG0806

SEQ ID NO. 5601

STRAIN 2603

aagaagcttactttttatttgggatttagatgggacattaatagattcgta
 tgtaccaattatggaagctcttgaagaaacctatcgtcatttttggttaa
 tatttgataaagaattaatccatgaatatattttacaggaatcagtgagg
 aaattatttggtaaacctttcagaggaagagcaaatacctcatgaaaaact
 gaaagcatattttacaaaagaacaagaaagtcgagattctaaaatacatt
 taatgccatatgcaaaagagattttagaatggaccaaagaacaagatatc
 cccaattttatgtatacacataaaggagcaagtacgcattcagtggttga
 aaccttgacagatctctcattattttgatgaaattttaactggtgttcgg
 gattcgagcgaaaaccacatccacaagggattaattatttagttaaacga
 tattcttttagataaatcaatgacttattacataggagatcgccactaga
 tttggaggttgctcaaaatgctggtataaaatccataaacttaaggtag
 agaattccaaagaaaactataatatttcaagtcctcaaagatataatatca
 cttgatttcactcgtttggat

SEQ ID NO. 5602

STRAIN COH1

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAA
 TAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCAT
 TTTGGCTTAATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGA
 ATCAGTGGGGCAATTATTGGTAAACCTTTAGAGGAAGAGCAAATACCTC
 ATGAAAAACTGAAAGCATA'TTTACAAAAGAACAAGAAAGTCGAGATTCT
 AAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGA
 ACAAGATATTCCTCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
 CAGTGTTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACT
 GGTGTTTCGGGATTCGAGCGAAAACCATCCACAAGGGATTAATTATTT
 AGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATC
 GTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAAC
 TTAAGGTTAGAGAATTCCAAAGAAAACCTATAATATTTCAAGTCTCAAAGA
 TATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5603

STRAIN A909

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAAAT
 AGATTTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATT
 ATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT
 AAACCTTTTACAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTT
 ACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTT
 GACCAAAGAACAAGATATCCCCAATTTTATGTATACACATAAAGGAGCAAGT
 AGTGTTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACTGGT
 ATTCGAGCGAAAACCATCCACAAGGGATTAATTATTTAGTTAAACGATATTC
 TTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAG
 GTTGCTCAAAATGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATTC
 CCAAAGAAAACCTATAATATTTCAAGTCTCAAAGATATAATATCACTTGATTT
 CACTCGT

SEQ ID NO. 5604

STRAIN H36B

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAAATAGATTTCG
 TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAA
 TATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT
 TATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATAT
 TTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATG
 CAAAAGAGATTTTAGAATGGACCAAAGAACCTTGCAGATCTCTCATTATTTT
 ATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGAT
 TAATTATTTAGTTAAACGATATTCCTTTAGATAAATCAATGACTTATTACATAG
 GAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAA
 CTTAAGGTTAGAGAATTCCAAAGAAAACCTATAATATTTCAAGTCTCAAAGAT
 ATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5605

STRAIN 18RS21

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAAATAGATT
 CGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAA
 TATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT
 TATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATAT
 TTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATG
 CAAAAGAGATTTTAGAATGGACCAAAGAACCTTGCAGATCTCTCATTATTTT
 ATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGAT
 TAATTATTTAGTTAAACGATATTCCTTTAGATAAATCAATGACTTATTACATAG
 GAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAA
 CTTAAGGTTAGAGAATTCCAAAGAAAACCTATAATATTTCAAGTCTCAAAGAT
 ATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5606

STRAIN M732

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAAATAGAT
 TCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAA
 TATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAAT
 TATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATAT
 TTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATG
 CAAAAGAGATTTTAGAATGGACCAAAGAACCTTGCAGATCTCTCATTATTTT
 ATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGAT
 TAATTATTTAGTTAAACGATATTCCTTTAGATAAATCAATGACTTATTACATAG
 GAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAA
 CTTAAGGTTAGAGAATTCCAAAGAAAACCTATAATATTTCAAGTCTCAAAGAT
 ATAATATCACTTGATTTCACTCGTTTGGAT

Table 56: Comparative Sequences relating to SAG0806

TTGGAAACCTTGCAGATCTCTCATTATTTTGTATGAAATTTTAACTGGTGTTCGGGATT
 GAGCGAAAACCATCCACAAGGGATTAATTATTTAGTTAAACGATATTCCTTAGATAAA
 TCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGT
 ATAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTC
 AAAGATATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5607

STRAIN CJB110

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATT
 AATAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTT
 AATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTATT
 GGTAAACCTTTTACAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAA
 AGAACAAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGA
 ATGGACCAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCA
 TTCAGTGTGGAAACCTTGCAGATCTCTCATTATTTTATGATGAAATTTTAACTGGTGTTC
 TGGATTTCGAGCGAAAACCATCCACAAGGGATTAATTATTTAGTTAAACGATATTCCTT
 AGATAAATCAATGACTTATTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAAA
 TGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTTC
 AAGTCTCAAGGATATAATATCACTTGATTTCACTCGTT

SEQ ID NO. 5608

STRAIN 1169NT

aAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGTATGTACCAATTA
 TAGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAATCC
 ATGAATATATTTTACAGGAATCAGTGGGGAAATTTATTTGGTAAACCTTTTACAGGAAGAGC
 AAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTA
 AAATACATTTAATGCCATACGCAAAAGAGATTTTAGAATGGACCAAGAAACAAGATATCC
 CCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAAACCTTGCAGA
 TCTCTCATTATTTTATGATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATC
 CACAAGGGATTAATTAATTTAGTTAAACGATATTCCTTTAGATAAATCAATGACTTATTACA
 TAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAACT
 TAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGGATATAATATCAC
 TTGATTTCACTCGTTTGGAT

SEQ ID NO. 5609

STRAIN JM9130013

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGA
 TTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAATATT
 TGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTTATTGGTAAA
 CCTTTACAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAACA
 AGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGAC
 CAAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGT
 GTTGGAAACCTTGCAGATCTCTCATTATTTTATGATGAAATTTTAACTGGTGTTCGGGATT
 CGAGCGAAAACCATCCACAAGGGATTAATTAATTTAGTTAAACGATATTCCTTTAGATAA
 ATCAATGACTTATTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAAATGCTGG
 TATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCT
 CAAAGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5610

STRAIN 090

AAGAAGCTTACTTTTATTTGG
 GATTTAGATGGGACATTAATAGATTCGTATGTACCAATTATGGAAGCTCT
 TGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAATCC
 ATGAATATATTTTACAGGAATCAGTGGGGCAATTATTGGTAAACCTTTCA
 GAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGA
 ACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGA
 TTTTAGAATGGACCAAGAACAAGATATCCCAATTTTATGTATACACAT
 AAAGGAGCAAGTACGCATTTCAGTGTGGAAACCTTGCAGATCTCTCATT
 TTTTATGATGAAATTTTAACTGGTGTTCCTGGATTTCGAGCGAAAACCATC
 CACAAGGGATTAATTAATTTAGTTAAACGATATTCCTTTAGATAAATCAATG
 ACTTATTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAAATGC
 TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATA
 ATATTTCAAGTCTCAAGGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5611

STRAIN M781

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGT
 ATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA
 ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGG
 GCAATTATTGGTAAACCTTTTACAGGAAGAGCAAATACCTCATGAAAAAC
 TGAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACAT
 TTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAGAACAAGATAT
 TCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGG
 AAACCTTGCAGATCTCTCATTATTTTATGATGAAATTTTAACTGGTGTTCG
 GGATTTCGAGCGAAAACCATCCACAAGGGATTAATTAATTTAGTTAAACG
 ATATTTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCCTAG
 ATTTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAACTTAAGGTTA
 GAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGGATATAATATC
 ACTTGATTTCACTCGT

PRETTY of: /biotmp/msa45163.2{*} January 21, 2003 06:53 ..

Table 56: Comparative Sequences relating to SAG0806

	1				50
msa45163.2{240_18RS21}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_2603}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_A909}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_H36B}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_JM9130013}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_COH1}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M732}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M781}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_090}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_CJB110}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_1169NT}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
Consensus	*****	*****	*****	*****	*****
	51				100
msa45163.2{240_18RS21}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_2603}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_A909}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_H36B}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_JM9130013}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_COH1}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_M732}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_M781}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_090}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_CJB110}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
msa45163.2{240_1169NT}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGtTTAA
Consensus	*****	***-*****	*****	*****	*****-*****
	101				150
msa45163.2{240_18RS21}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_2603}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_A909}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_H36B}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_JM9130013}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_COH1}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_M732}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_M781}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_090}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_CJB110}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_1169NT}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa45163.2{240_18RS21}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_2603}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_A909}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_H36B}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_JM9130013}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_COH1}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M732}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M781}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_090}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_CJB110}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_1169NT}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
Consensus	-*****	*****	*****	*****	*****
	201				250
msa45163.2{240_18RS21}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_2603}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_A909}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_H36B}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_JM9130013}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_COH1}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M732}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M781}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTyT	AAAATACATT
msa45163.2{240_090}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_CJB110}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_1169NT}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
Consensus	*****	*****	*****	*****~*	*****
	251				300
msa45163.2{240_18RS21}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_2603}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_A909}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_H36B}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_JM9130013}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_COH1}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATt
msa45163.2{240_M732}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATt
msa45163.2{240_M781}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATt
msa45163.2{240_090}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_CJB110}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_1169NT}	TAATGCCATA	cGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
Consensus	*****	-*****	*****	*****	*****-

Table 56: Comparative Sequences relating to SAG0806

msa45163.2{240_18RS21}	301	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	350	CAGTGTGGA
msa45163.2{240_2603}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_A909}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_H36B}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_JM9130013}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_COH1}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_M732}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_M781}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_090}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_CJB110}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
msa45163.2{240_1169NT}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT		CAGTGTGGA
Consensus		*****	*****	*****	*****		*****
msa45163.2{240_18RS21}	351	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT	400	GGTGTTCgG
msa45163.2{240_2603}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_A909}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_H36B}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_JM9130013}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_COH1}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_M732}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_M781}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_090}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_CJB110}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
msa45163.2{240_1169NT}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTTAACT		GGTGTTCgG
Consensus		*****	*****	*****	*****		*****
msa45163.2{240_18RS21}	401	GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	450	AGTTAAACGA
msa45163.2{240_2603}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_A909}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_H36B}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_JM9130013}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_COH1}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_M732}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_M781}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_090}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_CJB110}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
msa45163.2{240_1169NT}		GATTTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT		AGTTAAACGA
Consensus		*****	*****	*****	*****		*****
msa45163.2{240_18RS21}	451	TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	500	GTCCaCTAGA
msa45163.2{240_2603}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_A909}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_H36B}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_JM9130013}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_COH1}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_M732}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_M781}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCaCTAGA
msa45163.2{240_090}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCcCTAGA
msa45163.2{240_CJB110}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCcCTAGA
msa45163.2{240_1169NT}		TATTCTTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC		GTCCcCTAGA
Consensus		*****	*****	*****	*****		*****
msa45163.2{240_18RS21}	501	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	550	TTAAGGTTAG
msa45163.2{240_2603}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_A909}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_H36B}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_JM9130013}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_COH1}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_M732}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_M781}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_090}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_CJB110}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
msa45163.2{240_1169NT}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC		TTAAGGTTAG
Consensus		*****	*****	*****	*****		*****
msa45163.2{240_18RS21}	551	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA	600	TATAATATCA
msa45163.2{240_2603}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_A909}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_H36B}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_JM9130013}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_COH1}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_M732}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_M781}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_090}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_CJB110}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA
msa45163.2{240_1169NT}		AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA		TATAATATCA

Table 56: Comparative Sequences relating to SAG0806

Consensus	*****	*****	*****	*****-*	*****
	601		621		
msa45163.2{240_18RS21}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_2603}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_A909}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_H36B}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_JM9130013}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_COH1}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_M732}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_M781}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_090}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_CJB110}	CTTGATTTC	CTCGTt-----	-		
msa45163.2{240_1169NT}	CTTGATTTC	CTCGTttgga	t		
Consensus	*****	*****	-----	-	

SEQ ID NO. 5612

STRAIN 2603 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5613

STRAIN A909 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5614

STRAIN H36B frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5615

STRAIN 18RS21 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5616

STRAIN M732 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5617

STRAIN COH1 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5618

STRAIN CJB110 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5619

STRAIN 1169NT frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5620

STRAIN JM9130013 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5621

STRAIN 090 frame: 1

KKLTFIWDLDGTLIDSYVPIMEALEETRYRHFGGLIFDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO

Table 56: Comparative Sequences relating to SAG0806

ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5622

STRAIN M781 frame: 1

KKLTFIWDLDGTLIDSYVPI MEALEETRYH FGLIFDKELI HEYILQESVG QLLVNLSEEE
 QIPHEKCLKAYFTKEQESRDXKIHLMPYAKE ILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

PRETTY of: /biotmp/msa45645.2{*} January 21, 2003 06:57 ..

	1				50
msa45645.2{240_18RS21}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_A909}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_JM9130013}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_2603}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_H36B}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_090}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_CJB110}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_M781}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_COH1}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_M732}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_1169NT}	KKLTFIWDLD	GTIDSYVPI	MEALEETRYH	FGLIFDKELI	HEYILQESVG
Consensus	*****	*****	*****	*****	*****
	51				100
msa45645.2{240_18RS21}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_A909}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_JM9130013}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_2603}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_H36B}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_090}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_CJB110}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_M781}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_COH1}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_M732}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_1169NT}	KLVLNLSEEE	QIPHEKCLKAY	FTKEQESRDS	KIHLMPYAKE	ILEWTKEQDI
Consensus	*****	*****	*****	*****	*****
	101				150
msa45645.2{240_18RS21}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_A909}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_JM9130013}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_2603}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_H36B}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_090}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_CJB110}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_M781}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_COH1}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_M732}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
msa45645.2{240_1169NT}	PNFMYTHKGA	STHSVLETLO	ISHYFDEILT	GVSGFERKPH	PQGYNILVVKR
Consensus	*****	*****	*****	*****	*****
	151				200
msa45645.2{240_18RS21}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_A909}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_JM9130013}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_2603}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_H36B}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_090}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_CJB110}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_M781}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_COH1}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_M732}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
msa45645.2{240_1169NT}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLENSKENY	NISSLKDIIS
Consensus	*****	*****	*****	*****	*****
	201				
msa45645.2{240_18RS21}	LDFTRld				
msa45645.2{240_A909}	LDFTR--				
msa45645.2{240_JM9130013}	LDFTR--				
msa45645.2{240_2603}	LDFTRld				
msa45645.2{240_H36B}	LDFTRld				
msa45645.2{240_090}	LDFTR--				
msa45645.2{240_CJB110}	LDFTR--				
msa45645.2{240_M781}	LDFTR--				
msa45645.2{240_COH1}	LDFTRld				
msa45645.2{240_M732}	LDFTRld				
msa45645.2{240_1169NT}	LDFTRld				
Consensus	*****				

Table 57: Comparative Sequences relating to SAG 1488**SEQ ID NO: 5701****STRAIN 2603**

ATGCTTATGACAAAAATAATAGGACTGACAGGAGGGATAGCTTCT
 GGAAAGTCAACGGTAACAAAAATAATACGAGAATCAGGTTTTAAAGTCATAGATGCGGAT
 CAAGTGGTTCATAAATTGCAAGCTAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGG
 TTGGGTCCCGAGATACTTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATG
 ATTTTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTCGT
 CAAGAGTTAGCATGTGACGCGACCAATTA AAAACAAACAGAAGAGATATTTTTCATGGAT
 ATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTGATGAGATTTGGTTGGTATTT
 GTTGATAAAGAAAAACAATTACAACGATTAAATGGCCCGTAACAACTACAGTCGAGAAGAA
 GCAGAATTACGACTTTCACACCAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTT
 ATTATTGACAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
 CGTTTA

SEQ ID NO: 5702**STRAIN 090**

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAG
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT
 TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTG
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 CGTCAAGAGTTAGCATGTGACGCGACCAATTA AAAACAAACAGAAGAGAT
 ATTTTTCGTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 ACACCAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA
 ATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
 CAACGTTTA

SEQ ID NO: 5703**STRAIN A909**

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAG
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT
 TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTG
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 CGTCAAGAGTTAGCATGTGACGCGACCAATTA AAAACAAACAGAAGAGAT
 ATTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
 TTAATGGCCCGTAAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 ACACCAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTG
 ACAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
 CAACGTTTA

SEQ ID NO: 5704**STRAIN H36B**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGC
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTC
 GTCAAGAGTTAGCATGTGACGCGACCAATTA AAAACAAACAGAAGAGATA
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAAACAACTACAGTCGAGAAGAAGCGGAATTACGACTTTC
 CACCAAATACCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA
 TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTC
 AACGTTTA

SEQ ID NO: 5705**STRAIN 18RS21**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGC
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTC
 GTCAAGAGTTAGCATGTGACGCGACCAATTA AAAACAAACAGAAGAGATA
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 CACCAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA
 CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTC
 AACGTTTA

SEQ ID NO: 5706**STRAIN M732**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGGT
 GGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTGA
 TGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGCTA
 ATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTCGT
 CAAGAGTTAGCATGTGACGCGACCAATTA AAAACAAACAGAAGAGATATT

Table 57: Comparative Sequences relating to SAG 1488

TTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTG
 ATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGATTA
 ATGGCCCGTAACAACCTACAGTCGAGAAGAAGCAGAATTACGACTTTCACA
 CCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGACA
 ATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
 CGTTTA

SEQ ID NO: 5707**STRAIN COH1**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG
 TGGGAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG
 ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGCT
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCCG
 TCAAGAGTTAGCATGTGAGCGCGACCAATTAAAACAAACAGAAGAGATAT
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
 GATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGATT
 AATGGCCCGTaACAACCTACAGTCGAGAAGAAGCAGAATTACGACTTTCAC
 ACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGAC
 AATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCA
 ACGTTTA

SEQ ID NO: 5708**STRAIN M781**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
 GTGGGAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGC
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTC
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAACAAACAGAAGAGATA
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAACAACCTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 CACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
 CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTC
 AACGTTTA

SEQ ID NO: 5709**STRAIN CJB110**

AAGTCAACGGTAACAAAAATAATACGAGAA
 TCAGGTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGC
 TAAGGTTGGGAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGA
 TACTTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATT
 TTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTAT
 CATTCTGTCAGAGTTAGCATGTGAGCGCGACCAATTAAAACAAACAGAAG
 AGATATTTTCGTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAA
 TGGTTTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACA
 ACGATTAATGGCCCGTaACAACCTACAGTCGAGAAGAAGCAGAATTACGAC
 TTTCACACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATT
 ATTAATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGC
 TCTTCAACGTTTA

SEQ ID NO: 5710**STRAIN 1169NT**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
 GTGGGAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGC
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTC
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAACAAACAGAAGAGATA
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAACAACCTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
 TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTC
 AACGTTTA

SEQ ID NO: 5711**STRAIN JM9130013**

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG
 TGGGAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG
 ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGCT
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCCG
 TCAAGAGTTAGCATGTGAGCGCGACCAATTAAAACAAACAGAAGAGATAT
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
 GATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGATT
 AATGGCCCGTAACAACCTACAGTCGAGAAGAAGCGGAATTACGACTTTCAC
 ACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGAT
 AATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTCA
 ACGTTTA

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221059.2{*} February 10, 2003 07:07 ..

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1                                     50
msa221059.2{245_H36B} -----AA
msa221059.2{245_JM9130013} -----AA
msa221059.2{245_1169NT} -----AA
msa221059.2{245_090} -----AA
msa221059.2{245_CJB110} -----AA
msa221059.2{245_18RS21} -----AA
msa221059.2{245_2603} atgcttatga caaaaataat aggactgaca ggagggatag cttctggaAA
msa221059.2{245_A909} -----AA
msa221059.2{245_COH1} -----AA
msa221059.2{245_M732} -----AA
msa221059.2{245_M781} -----AA
Consensus *****

51                                     100
msa221059.2{245_H36B} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_JM9130013} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_1169NT} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_090} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_CJB110} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_18RS21} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_2603} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_A909} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_COH1} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_M732} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
msa221059.2{245_M781} GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTAAAG GTCATAGATG
Consensus *****

101                                    150
msa221059.2{245_H36B} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_JM9130013} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_1169NT} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_090} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_CJB110} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_18RS21} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_2603} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_A909} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_COH1} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_M732} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_M781} CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
Consensus *****

151                                    200
msa221059.2{245_H36B} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_JM9130013} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_1169NT} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_090} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_CJB110} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_18RS21} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_2603} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_A909} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_COH1} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_M732} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_M781} GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
Consensus *****

201                                    250
msa221059.2{245_H36B} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_JM9130013} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_1169NT} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_090} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_CJB110} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_18RS21} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_2603} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_A909} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_COH1} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_M732} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_M781} GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
Consensus *****

251                                    300
msa221059.2{245_H36B} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_JM9130013} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_1169NT} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_090} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_CJB110} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_18RS21} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_2603} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_A909} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_COH1} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_M732} AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT

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Table 57: Comparative Sequences relating to SAG 1488

msa221059.2{245_M781}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
Consensus	*****	*****	*****	*****	*****
	301				350
msa221059.2{245_H36B}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_JM9130013}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_1169NT}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_090}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_CJB110}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_18RS21}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_2603}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_A909}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_COH1}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M732}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M781}	CAGCGCGACC	AATTAAAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
Consensus	*****	*****	*****	*****	*****
	351				400
msa221059.2{245_H36B}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_JM9130013}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_1169NT}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_090}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_CJB110}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_18RS21}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_2603}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_A909}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_COH1}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_M732}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
msa221059.2{245_M781}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTGTTGG
Consensus	*****	*****	*****	*****	*****
	401				450
msa221059.2{245_H36B}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_JM9130013}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_1169NT}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_090}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_CJB110}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_18RS21}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_2603}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_A909}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_COH1}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M732}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M781}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
Consensus	*****	*****	*****	*****	*****
	451				500
msa221059.2{245_H36B}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_JM9130013}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_1169NT}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_090}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_CJB110}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_18RS21}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_2603}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_A909}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_COH1}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M732}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M781}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
Consensus	*****	*****	*****	*****	*****
	501				550
msa221059.2{245_H36B}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAtAATAAT	GGTGATTAA
msa221059.2{245_JM9130013}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAtAATAAT	GGTGATTAA
msa221059.2{245_1169NT}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAtAATAAT	GGTGATTAA
msa221059.2{245_090}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TaAtAATAAT	GGTGATTAA
msa221059.2{245_CJB110}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TaAtAATAAT	GGTGATTAA
msa221059.2{245_18RS21}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAcAATAAT	GGTGATTAA
msa221059.2{245_2603}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAcAATAAT	GGTGATTAA
msa221059.2{245_A909}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAcAATAAT	GGTGATTAA
msa221059.2{245_COH1}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAcAATAAT	GGTGATTAA
msa221059.2{245_M732}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAcAATAAT	GGTGATTAA
msa221059.2{245_M781}	AGATAAAAAA	AGTTTCGCTA	GTCTTATTAT	TgAcAATAAT	GGTGATTAA
Consensus	*****	*****	*****	*****	*****
	551				591
msa221059.2{245_H36B}	TAACCTTTAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_JM9130013}	TAACCTTTAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_1169NT}	TAACCTTTAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_090}	TAACCTTTAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_CJB110}	TAACCTTTAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_18RS21}	TAACCTTTAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_2603}	TAACCTTTAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_A909}	TAACCTTTAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_COH1}	TAACCTTTAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A

Table 57: Comparative Sequences relating to SAG 1488

msa221059.2{245_M732}	TAAC	TTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_M781}	TAAC	TTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
Consensus	*****	*****	*****	*****	*****	*

SEQ ID NO: 5712

STRAIN 2603 frame: 1

MLMTKIIIGLTGGIASGKSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI
LDADGELDRPKLSQMI FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI
EEKYIKWFDEIWLWVFDKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNN
GDLITLKEQILDALQRL

SEQ ID NO: 5713

STRAIN 090 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQ
L

SEQ ID NO: 5714

STRAIN A909 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

SEQ ID NO: 5715

STRAIN H36B frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ
L

SEQ ID NO: 5716

STRAIN 18RS21 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

SEQ ID NO: 5717

STRAIN M732 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

SEQ ID NO: 5718

STRAIN COH1 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

SEQ ID NO: 5719

STRAIN M781 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

SEQ ID NO: 5720

STRAIN CJB110 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQ
L

SEQ ID NO: 5721

STRAIN 1169NT frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ
L

SEQ ID NO: 5722

STRAIN JM9130013 frame: 1

KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQRDQLKQTEEIFFMDIPLLI EEEKYIKWFDEIWLWV
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ
L

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221398.2(*) February 10, 2003 07:15 ..

	1				50
msa221398.2{245_090}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_CJB110}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_1169NT}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_H36B}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_JM9130013}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_18RS21}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_2603}	mlmtkiiglt ggiasgKSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_A909}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_COH1}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_M732}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
msa221398.2{245_M781}	-----KSTV	TKIIRESGFK	VIDADQVVHK	LQAKGGKLYQ	
Consensus	*****	*****	*****	*****	*****
	51				100
msa221398.2{245_090}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_CJB110}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_1169NT}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_H36B}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_JM9130013}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_18RS21}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_2603}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_A909}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_COH1}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_M732}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
msa221398.2{245_M781}	ALLEWLGPEI	LDADGELDRP	KLSQMIFANP	DNMKT SARLQ	NSII RQELAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa221398.2{245_090}	QRDQLKQTEE	IFFvDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_CJB110}	QRDQLKQTEE	IFFvDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_1169NT}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_H36B}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_JM9130013}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_18RS21}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_2603}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_A909}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_COH1}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_M732}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
msa221398.2{245_M781}	QRDQLKQTEE	IFFmDIPLLI	EEKYIKWFDE	IWLVFVDKEK	QLQRLMARNN
Consensus	*****	***-*****	*****	*****	*****
	151				197
msa221398.2{245_090}	YSREEAELRL	SHQmPLTDKK	SFASLIInNN	GDLITLKEQi	LDALQRL
msa221398.2{245_CJB110}	YSREEAELRL	SHQmPLTDKK	SFASLIInNN	GDLITLKEQi	LDALQRL
msa221398.2{245_1169NT}	YSREEAELRL	SHQiPLTDKK	SFASLIIdNN	GDLITLKEQm	LDALQRL
msa221398.2{245_H36B}	YSREEAELRL	SHQiPLTDKK	SFASLIIdNN	GDLITLKEQm	LDALQRL
msa221398.2{245_JM9130013}	YSREEAELRL	SHQiPLTDKK	SFASLIIdNN	GDLITLKEQm	LDALQRL
msa221398.2{245_18RS21}	YSREEAELRL	SHQmPLTDKK	SFASLIIdNN	GDLITLKEQi	LDALQRL
msa221398.2{245_2603}	YSREEAELRL	SHQmPLTDKK	SFASLIIdNN	GDLITLKEQi	LDALQRL
msa221398.2{245_A909}	YSREEAELRL	SHQmPLTDKK	SFASLIIdNN	GDLITLKEQi	LDALQRL
msa221398.2{245_COH1}	YSREEAELRL	SHQmPLTDKK	SFASLIIdNN	GDLITLKEQi	LDALQRL
msa221398.2{245_M732}	YSREEAELRL	SHQmPLTDKK	SFASLIIdNN	GDLITLKEQi	LDALQRL
msa221398.2{245_M781}	YSREEAELRL	SHQmPLTDKK	SFASLIIdNN	GDLITLKEQi	LDALQRL
Consensus	*****	***-*****	*****-*	*****-	*****

Table 58: Comparative Sequences relating to SAG0182

SEQ ID NO. 5801

STRAIN 2603

ATGTTGATGGTGTGTTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCTTTTTATTG
 GTAAATAATAGTTATTTTAGACAGTTAATTGAAGAGCGGTCTAAACGTGAAACGGTAGTC
 CTTGTCATCATTTTCGGCTTGTTTGTTAFTATATCTAATATAACAGGAATTGAAATAAAA
 GGGGATCGAAGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTT
 GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTGGTTGGA
 TCAATTGTTGGTTTATTGGAGGAGTTCATCGCTTTTTTCAAGGAAGCTTTTCAGGTTCT
 TTCTATATTGTCAGTTCAGTTCTAGTCGGCATTGTTAGCGGAAAGATTGGTGATAAGCTT
 AAGGAAAACCATCTCTACCCCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAA
 AGTATCCAGATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAAATGATTGTC
 ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGCGATTTTGAAAACCT
 TATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTTGAATTGACT
 CGACAGACTCTGCCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGC
 GAAATFATAAAGAGGCATACTAACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTA
 TTAGCTCATATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGAC
 TTATCTAAAAGTGTTATTTTTGATGGCGAACCAGAATTGCGCAAGATAAAGCGGCGATT
 TCTTGTCCAGATCACAACCTGTCAGTTAAATTCTGCTATTGTAGTTCTCTAAAAATAAAT
 GATAAAACTGTGGGTGCCCTTAAAAATGTACTTTGCAGGAGATAAGACAATGTCTGAGGTG
 GAGGAAAACCTAGTCCTTGGTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATA
 ACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC
 AACCTCAITTTCTTCTTTAATGCCATTAAACACAATTAGTGCAATTAATCCGTATTGATTCT
 GATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTTAGAACAAGTTTGCAGGGT
 GGTGAGGATCGTGAGGTAAACGCTTGAGCAAGAAAAATCACATGTGGATGCTTATATGAAT
 GTTGAAAAATTACGTTTCCCTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAA
 AAAATGAAGTTACCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCT
 TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGTCATTAT
 TATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATACTATCATTTGATAAATTA
 GGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAAC
 AGGCTGAATTTATTATATGGTAGTGTAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGT
 ACAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTAAT
 TCT

SEQ ID NO. 5802

STRAIN 090

TTGATGGTGTGTTGTTATTCCAAAGGCTAGGAATTATTAT
 GATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
 AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCTATCATTTTCGGCTTG
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAG
 TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTTCTGACTCACTTG
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTCATCGCTTTTTTCA
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGGCA
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCT
 TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
 GCTATTTGTTGGTATTTTACAGGATGGGAACCTTGTCAAAATGATTTGTCA
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGCGATT
 TTGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT
 TGACACCGCAATCTGCTAGGAGCGTTTGCGAAAATTATAAAGAGGCATACT
 AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
 TGGTGTGGCCATGATCACCATATTGCAGGACAACCAAGTCAAACAGACC
 TATCTAAAAGTGTTATTTTGTATGGCGAACCAGAATTGCGCAAGATAAA
 GCGGCGATTTCTTGTCCAGATCACAACCTGTCAGTTAAATTTCTGCTATTGT
 AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT
 TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGT
 TTAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
 AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTACAAGCACAAATCA
 ACCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCAATTAATCCGT
 ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT
 TAGAACAAGTTTGCAGGTGGTCAAGGTGAGTCAAGGTAAACGCTTGAGCAAG
 AAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
 GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTT
 ACCGCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTAGACATGCTT
 TCAAAGAACGTAAGACGACCAACCATATATTGGTTCAAATAAAGCCAGAT
 GGTCAATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
 AGTGTAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTAATT
 CT

SEQ ID NO. 5803

STRAIN A909

TTGATGGTGTGTTGTTATTCCAAAGGCTAGGAATTATTAT
 GATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
 AAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCTATCATTTTCGGCTTG
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAG
 TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTG
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTCATCGCTTTTTTCA
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGGCA
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCT

Table 58: Comparative Sequences relating to SAG0182

TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
 GCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAATGATTGTCA
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
 TTGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTT
 TGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACT
 AACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
 TGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACT
 TATCTAAAAGTGTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAA
 GCGGCGATTTCTTGTCAGATCACAACCTGTCAGTTAAATTCTGCTATTGT
 AGTTCCTCTAAAAATAAATGATAAACTGTGGGTGCCTTAAAAATGTACT
 TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGTT
 TTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
 AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
 ACCCTCATTTCTTCTTAATGCCATTAAACACAATTAGTGCATTAATCCGT
 ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT
 TAGAACAAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
 GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT
 ACCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCTT
 TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
 GGTCAATFATFATTTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
 AGTGTAAAGTTGCCCTTCATTTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT
 CT

SEQ ID NO. 5804

STRAIN H36B

TTGATGGTGTGTTATTTCCAAAGGCTAGGAATTATTATG
 ATTTTAGCCCTTTTTATTGGTAAATAATAGTTATTTAGACAGTTAATTGA
 AGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTTGT
 TTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAGT
 TTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTGC
 TAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTC
 TGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTTCAA
 GGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTAGTTCTAGTCGGCAT
 TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT
 CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG
 CTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAATGATTGTGAT
 TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
 TGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
 GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT
 GACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACTA
 ACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATATT
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT
 ATCTAAAAGTGTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAAG
 CGGCGATTTCTTGTCAGATCACAACCTGTCAGTTAAATTCTGCTATTGTA
 GTTCCTCTAAAAATAAATGATAAACTGTGGGTGCCTTAAAAATGTACTT
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGTT
 TAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAA
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCAA
 CCTTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAATCCGT
 TTGATTTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT
 AGAACAAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGA
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
 ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTA
 CCACCTTTTGGTTTACAGGTAAGTTAGAGAATGCAGTTTCGACATGCTTT
 CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
 ACTATCATTTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
 GTGTAAGTTGCCCTTCATTTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC
 T

SEQ ID NO. 5805

STRAIN 18RS21

TTGATGGTGTGTTATTTCCAAAGGCTAGGAATTATTATG
 ATTTTAGCCCTTTTTATTGGTAAATAATAGTTATTTAGACAGTTAATTGA
 AGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTTGT
 TTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAGT
 TTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTGC
 TAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTC
 TGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTTCAA
 GGAAGCTTTTTCAGGTTCTTTCTATATTGTGAGTTAGTTCTAGTCGGCAT
 TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT
 CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG
 CTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAATGATTGTGAT
 TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
 TGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
 GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT

Table 58: Comparative Sequences relating to SAG0182

GACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACTA
 ACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT
 ATCTAAAAGTGTTATTTTGGATGGCGAACCAAGaATTGCGCAAGATAAAG
 CGGCGATTTCTTGTCCAGATCACAACCTGTCAGTTAAATTCTGCTATTGTA
 GTTCCTCTAAAAATAAATGATAAACTGTGGGTGCCTTAAAAATGTACTT
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGTT
 TAGCGCAAATATTTTCAGGACAACCTGGCAATGGCGATAACAGAGGAACAA
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCAA
 CCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCAATTAATCCGTA
 TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT
 AGAACAAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGA
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
 ATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTTA
 CCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCTTT
 CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
 GTCATTATTATTGTGTTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
 ACTATCATTGATAAATTAGGTCAAGAAAACAGTTGCAGAGAGTAAGGGTAC
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
 GTGTAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTGG
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTCT
 T

SEQ ID NO. 5806

STRAIN M732

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGAT
 TTTAGCCTTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTGAAG
 AGCGGTCTAAACGTGAAACGGTAGTCCTTGTCTATCATTTTTCGGCTTGTTT
 GTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGTTT
 GGTGCGAGCGCCCTTTTCTAACCAACGATTTCCCATTTCTGACTCATTGCTA
 ATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTG
 GTTGGATCAATTGTTGGTTTATTGAGGAGTTTCATCGCTTTTTTCAAGG
 AAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGGCATTG
 TTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCTTCA
 ACAAGCCAAGTTATTTAATTAGTATTTATTTGCCGAAAGTATCCAGATGCT
 ATTTGTTGGCATTTTTTACAGGATGGGAACTTGTCAAATGATTGTCAATC
 CAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCCTTGGGATTTTG
 AAAACTTATTTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGA
 TGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTTGA
 CACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACTAAC
 TTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATTGG
 TATTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTTAT
 CTAAAAGTGTTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAAGCG
 GCGAATTTCTTGTCCAGATCACAACCTGTCAGTTAAATTCTGCTATTGTAGT
 TCCTCTAAAAATAAATGATAAACTGTGTGTGCCTTAAAAATGTACTTTG
 CAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGTTTA
 GCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAAAA
 TAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCAACC
 CTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCAATTAATCCGTATT
 GATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTTAG
 AACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGAAA
 AATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTGAT
 AAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTTACC
 GCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCTTTCA
 AAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGT
 CATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATAC
 TATCATTGATAAATTAGGTCAAGAAAACAGTTGCAGAGAGTAAGGGGACAG
 GTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTAGT
 GTAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTGGTA
 TCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTCT

SEQ ID NO. 5807

STRAIN COH1

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTAT
 TATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAA
 TTGAAGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCTATCATTTTTCGGC
 TTGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCG
 AAGTTTGGTCGAGCGCCCTTTTCTAACCAACGATTTCCCATTTCTGACTCAC
 TTGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGGA
 CCTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT
 TCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCTAGTTCTAGTCTG
 GCATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTAC
 CCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCGCAAGATATCCA
 GATGCTATTTGTTGGCAITTTTACAGGATGGGAACTTGTCAAATGATTG
 TCATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGC
 ATTTTGAAAACITATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAAC
 GAGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAG
 GTTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCAT
 ACTAACCTTGTGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCA
 TATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAG
 ACTTATCTAAAAGTGTTATTTTGTATGGCGAACCAAGAATTGCGCAAGAT
 AAAGCGGCGATTTCTTGTCCAGATCACAACCTGTCAGTTAAATTCTGCTAT
 TGTAGTTCTCTAAAAATAAATGATAAACTGTGTGTGCCTTAAAAATGT

Table 58: Comparative Sequences relating to SAG0182

ACTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAAACCTAGTCCTT
GGTTTAGCGCAAATATTTTTCAGGACAACTGGCAATGGGGATAACAGAGGA
ACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAA
TCAACCCTCATTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATC
CGTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTT
TTTTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGC
AAGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTC
CCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAA
GTTACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATG
CTTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCA
GATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTC
AGATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGG
GGACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATAT
GGTAGTGTAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGT
TTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTA
ATTCT

SEQ ID NO. 5808

STRAIN M781

TTGATGGTGGTTGTTATTCCAAAGGCTAGGAATTATTA
TGATTTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATT
GAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTTCATCATTTCGGCTT
GTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAA
GTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTTCTGACTCACTT
GCTAATAACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGACC
TCTGGTTGGATCAATTGTTGGTTTATTGAGGAGTTTCATCGCTTTTTTC
AAGGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCGGC
ATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCC
TTCAACAAGCCAAGTTATTTAATTAGTATTATTTGCCGAAAGTATCCAGA
TGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGTG
ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGAT
TTTGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGA
GAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGT
TTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATAC
TAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATA
TTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGAC
TTATCTAAAAGTGTTATTTTGGATGGCGAACCAGAAATTGCGCAAGATAA
AGCGGCGATTTCTTGTCCAGATCACAACTGTTCAGTTAAATTTCTGCTATTG
TAGTTCTCTAAAATAAATGATAAACTGTGTGTGCCTTAAAATGTAC
TTTGACAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGG
TTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAAC
AAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC
AACCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAATCCG
TATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTT
TTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAA
GAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCC
TGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGT
TACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCT
TTCAAAGAACCTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGA
TGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAG
ATACTATCATTGATAAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGG
ACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGG
TAGTGTAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTT
GGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT
TCT

SEQ ID NO. 5809

STRAIN CJB110

TTGATGGTGGTTGTTATTCCAAAGGCTAGGAATTATTAT
GATTTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTTCATCATTTCGGCTTG
TTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTTCTGACTCACTTG
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGACCT
CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCGGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCTT
TCAACAAGCCAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGAT
GCTATTTGTTGGTATTTTACAGGATGGGAACCTGTCAAATGATTGTCA
TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGAT
TTGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGT
TGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACT
AAGTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
TGGTGTGGCCATGATCACCATATTGCAGGACAACCGTCAAACAGACC
TATCTAAAAGTGTTATTTTGGATGGCGAACCAGAAATTGCGCAAGATAAA
GCGGCGATTTCTTGTCCAGATCACAACTGTTCAGTTAAATTTCTGCTATTGT
AGTTCTCTAAAATAAATGATAAACTGTGGGTGCCCTTAAAATGTACT
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGT
TTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
ACCCTCATTTTTTCTTTAATGCCATTAAACACAATTAGTGCATTAATCCGT
ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT

Table 58: Comparative Sequences relating to SAG0182

TAGAACAAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
 GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT
 ACCGCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTAGACATGCTT
 TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
 GGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
 TACTATCATTGATAAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
 AGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT
 CT

SEQ ID NO. 5810

STRAIN 1169NT

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATT
 ATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAAT
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCTATCATTTTTCGGCT
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA
 AGTTTGGTTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACT
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTT
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGG
 CATTGTGAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
 CTTCACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAG
 ATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAATGATTGT
 CATTCCAATGATGATTTTTAAATAGTTTAGGTTCCACACTTTTCTTGCGA
 TTTTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACG
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG
 TTTGACACCGCAATCTGCTAGGAGCGTTTTCGAAATTATAAAGAGGCATA
 CTAATTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACAGTCAAACAGA
 CCTATCTAAAAGTGTATTTTTTGATGGCGAACCAAGAATTGCGCAAGATA
 AAGCGGCGATTTCTTGTCCAGATCACAACGTGTCAGTTAAATTCTGCTATT
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCTTAAAAATGTA
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTG
 GTTTAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT
 CAACCTCATTTCTTTAATGCCATTAAACAAATTAGTGCATTAATCC
 GTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
 TTTAGAACAAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCA
 AGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
 CTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAG
 TTACCGCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGC
 TTTTAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG
 ATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA
 GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG
 TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
 GTAGTGAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTT
 TGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAA
 TTCT

SEQ ID NO. 5810

STRAIN JM9130013

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATT
 ATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAAT
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCTATCATTTTTCGGCT
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA
 AGTTTGGTTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACT
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTT
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGG
 CATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAG
 ATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAATGATTGT
 CATTCCAATGATGATTTTTAAATAGTTTAGGTTCCACACTTTTCTTGCGA
 TTTTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACG
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG
 TTTGACACCGCAATCTGCTAGGAGCGTTTTCGAAATTATAAAGAGGCATA
 CTAACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGA
 CTTATCTAAAAGTGTATTTTTTGATGGCGAACCAAGAATTGCGCAAGATA
 AAGCGGCGATTTCTTGTCCAGATCACAACGTGTCAGTTAAATTCTGCTATT
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCTTAAAAATGTA
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTG
 GTTTAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT
 CAACCTCATTTCTTTAATGCCATTAAACAAATTAGTGCATTAATCC
 GTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
 TTTAGAACAAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCA
 agAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
 CTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAG
 TTACCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGC
 TTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG

Table 58: Comparative Sequences relating to SAG0182

ATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA
 GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG
 TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
 GTAGTGTAAGTTGCCTTTCAATTTTCGAGCGACAAGAATGGTACAAAAGTT
 TGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAA
 TTCT

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa442667.2(*) January 13, 2003 06:34 ..

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1                                     50
msa442667.2{248_18RS21} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_2603} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_A909} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_H36B} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_JM9130013} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_COH1} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M781} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M732} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_090} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_CJB110} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_1169NT} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
Consensus *****

51                                     100
msa442667.2{248_18RS21} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_2603} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_A909} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_H36B} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_JM9130013} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_COH1} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M781} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M732} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_090} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_CJB110} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_1169NT} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
Consensus *****

101                                    150
msa442667.2{248_18RS21} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_2603} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_A909} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_H36B} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_JM9130013} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_COH1} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M781} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M732} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_090} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_CJB110} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_1169NT} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
Consensus *****

151                                    200
msa442667.2{248_18RS21} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_2603} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_A909} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_H36B} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_JM9130013} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_COH1} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M781} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M732} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_090} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_CJB110} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_1169NT} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
Consensus *****

201                                    250
msa442667.2{248_18RS21} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_2603} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_A909} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_H36B} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_JM9130013} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_COH1} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M781} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M732} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_090} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_CJB110} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_1169NT} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
Consensus *****

251                                    300
msa442667.2{248_18RS21} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA
msa442667.2{248_2603} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA

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Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_A909}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_H36B}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_JM9130013}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_COH1}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M781}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M732}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_090}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_CJB110}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_1169NT}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
Consensus	*****	*****	*****	*****	*****
301					
msa442667.2{248_18RS21}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_2603}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_A909}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_H36B}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_JM9130013}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_COH1}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M781}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M732}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_090}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_CJB110}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
msa442667.2{248_1169NT}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTTCAAG	GAAGCTTTTC
Consensus	*****	*****	*****	*****	*****
351					
msa442667.2{248_18RS21}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_2603}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_A909}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_H36B}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_JM9130013}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_COH1}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_M781}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_M732}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_090}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_CJB110}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_1169NT}	AGGTTCTTTC	TATATTGTCA	GTTTCAGTTCT	AGTCGGCATT	GTgAGCGGAA
Consensus	*****	*****	*****	*****	**..*****
401					
msa442667.2{248_18RS21}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_2603}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_A909}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_H36B}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_JM9130013}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_COH1}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_M781}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_M732}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_090}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_CJB110}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
msa442667.2{248_1169NT}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTTC	AACAAGCCAA
Consensus	*****	*****	*****	*****	*****
451					
msa442667.2{248_18RS21}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_2603}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_A909}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_H36B}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_JM9130013}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_COH1}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M781}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M732}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_090}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_CJB110}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_1169NT}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
Consensus	*****	*****	*****	*****	*****
501					
msa442667.2{248_18RS21}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_2603}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_A909}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_H36B}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_JM9130013}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_COH1}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_M781}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_M732}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_090}	tATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_CJB110}	tATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
msa442667.2{248_1169NT}	cATTTTTCACA	GGATGGGAAC	TTGTCAAAAT	GATTGTTCATT	CCAATGATGA
Consensus	-*****	*****	*****	*****	*****
551					
msa442667.2{248_18RS21}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
600					

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_2603}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_A909}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_H36B}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_JM9130013}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_COH1}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M781}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M732}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_090}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_CJB110}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_1169NT}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_2603}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_A909}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_H36B}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_JM9130013}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_COH1}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M781}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M732}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_090}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_CJB110}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_1169NT}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_2603}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_A909}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_H36B}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_JM9130013}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_COH1}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M781}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M732}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_090}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_CJB110}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_1169NT}	ATTGACTCGA	CAGACTCTGC	CCTACCTtAG	ACAAGGTTTG	ACACCGCAAT
Consensus	*****	*****	*****-*	*****	*****
msa442667.2{248_18RS21}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_2603}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_A909}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_H36B}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_JM9130013}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_COH1}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_M781}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_M732}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_090}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_CJB110}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_1169NT}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
Consensus	*****	*****	*****	*****	-*****
msa442667.2{248_18RS21}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_2603}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_A909}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_H36B}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_JM9130013}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_COH1}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M781}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M732}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_090}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_CJB110}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_1169NT}	GTgGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
Consensus	**_*****	*****	*****	*****	**_*****
msa442667.2{248_18RS21}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_2603}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_A909}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_H36B}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_JM9130013}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_COH1}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_M781}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_M732}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_090}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_CJB110}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
msa442667.2{248_1169NT}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACtTA	TCTAAAAGTG
Consensus	*****	*****	****-*****	*****-*	*****

851

900

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_2603}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_A909}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_H36B}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_JM9130013}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_COH1}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_M781}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_M732}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_090}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_CJB110}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
msa442667.2{248_1169NT}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTCT
Consensus	*****	*****	*****	*****	*****
901					
msa442667.2{248_18RS21}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_2603}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_A909}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_H36B}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_JM9130013}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_COH1}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M781}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M732}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_090}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_CJB110}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_1169NT}	TGTCCAGATC	ACAACTGTCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
Consensus	*****	*****	*****	*****	*****
951					
msa442667.2{248_18RS21}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_2603}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_A909}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_H36B}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_JM9130013}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_COH1}	AATAAATGAT	AAAACCTGTGt	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M781}	AATAAATGAT	AAAACCTGTGt	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M732}	AATAAATGAT	AAAACCTGTGt	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_090}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_CJB110}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_1169NT}	AATAAATGAT	AAAACCTGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
Consensus	*****	*****	*****	*****	*****
1001					
msa442667.2{248_18RS21}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_2603}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_A909}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_H36B}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_JM9130013}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_COH1}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M781}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M732}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_090}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_CJB110}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_1169NT}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
Consensus	*****	*****	*****	*****	*****
1051					
msa442667.2{248_18RS21}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_2603}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_A909}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_H36B}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_JM9130013}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_COH1}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M781}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M732}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_090}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_CJB110}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_1169NT}	TTTTTCAGGAC	AACCTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
Consensus	*****	*****	*****	*****	*****
1101					
msa442667.2{248_18RS21}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_2603}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_A909}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_H36B}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_JM9130013}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_COH1}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M781}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M732}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_090}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_CJB110}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_1169NT}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
Consensus	*****	*****	*****	*****	*****
1150					
msa442667.2{248_18RS21}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_2603}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_A909}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_H36B}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_JM9130013}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_COH1}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M781}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M732}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_090}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_CJB110}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_1169NT}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	1151	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	1200	TGATTCTGAT
msa442667.2{248_2603}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_A909}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_H36B}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_JM9130013}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_COH1}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_M781}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_M732}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_090}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_CJB110}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
msa442667.2{248_1169NT}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCTGAT
Consensus		*****	*****	*****	*****		*****
msa442667.2{248_18RS21}	1201	AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT	1250	GAACAAGTTT
msa442667.2{248_2603}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_A909}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_H36B}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_JM9130013}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_COH1}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_M781}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_M732}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_090}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_CJB110}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
msa442667.2{248_1169NT}		AAAGCACGTT	ATGCACTGAT	GCAGTTAAGT	ACTTTTTTTT		GAACAAGTTT
Consensus		*****	*****	*****	*****		*****
msa442667.2{248_18RS21}	1251	GCAgGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	1300	AAATCACATG
msa442667.2{248_2603}		GCAgGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_A909}		GCAgGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_H36B}		GCAgGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_JM9130013}		GCAgGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_COH1}		GCAaGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_M781}		GCAaGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_M732}		GCAaGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_090}		GCAaGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_CJB110}		GCAaGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_1169NT}		GCAaGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
Consensus		***-*****	*****	*****	*****		*****
msa442667.2{248_18RS21}	1301	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	1350	TAAATATCAG
msa442667.2{248_2603}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_A909}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_H36B}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_JM9130013}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_COH1}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_M781}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_M732}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_090}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_CJB110}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_1169NT}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
Consensus		*****	*****	*****	*****		*****
msa442667.2{248_18RS21}	1351	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	1400	CaCCTTTTGG
msa442667.2{248_2603}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
msa442667.2{248_A909}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
msa442667.2{248_H36B}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
msa442667.2{248_JM9130013}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
msa442667.2{248_COH1}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CgCCTTTTGG
msa442667.2{248_M781}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CgCCTTTTGG
msa442667.2{248_M732}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CgCCTTTTGG
msa442667.2{248_090}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CgCCTTTTGG
msa442667.2{248_CJB110}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CgCCTTTTGG
msa442667.2{248_1169NT}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CgCCTTTTGG
Consensus		*****	*****	*****	*****	*-*****	
msa442667.2{248_18RS21}	1401	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc	1450	AAAGAACGTA
msa442667.2{248_2603}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_A909}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_H36B}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_JM9130013}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_COH1}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_M781}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_M732}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_090}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTaG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_CJB110}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTaG	ACATGCTTTc		AAAGAACGTA
msa442667.2{248_1169NT}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCTTTt		AAAGAACGTA
Consensus		*****	*****	*****-*	*****-..	*****	

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	1451	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_1169NT}		AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
Consensus		*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	1501	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_1169NT}		TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
Consensus		*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	1551	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
msa442667.2{248_1169NT}		TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC
Consensus		*****	*****	*****	*****-***	*****
msa442667.2{248_18RS21}	1601	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_1169NT}		TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
Consensus		*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	1651	CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_1169NT}		CTTCATTTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
Consensus		*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	1701	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_1169NT}		TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	

Table 58: Comparative Sequences relating to SAG0182

Consensus *****

SEQ ID NO. 5811

STRAIN 2603 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDAVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5812

STRAIN 090 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDAVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5813

STRAIN A909 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDAVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5814

STRAIN H36B frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDAVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5815

STRAIN 18RS21 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDAVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5816

STRAIN M732 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDAVGLTDRSNVLAHIGIGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5817

Table 58: Comparative Sequences relating to SAG0182

STRAIN COH1 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVLIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVKALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISTDIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5818

STRAIN M781 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVLIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVKALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISTDIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5819

STRAIN CJB110 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVLIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVKALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISTDIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5820

STRAIN 1169NT frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVLIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVKALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISTDIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5821

STRAIN JM9130013 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVLIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNCQLNSAIVVPLKINDKTVKALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISTDIIDKLGQETVAESKGTGTALVNLNNR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

PRETTY of: /biotmp/msa442834.2{*} January 13, 2003 06:47 ..

	1		50
msa442834.2{248_090}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_1169NT}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_18RS21}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_2603}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_A909}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_CJB110}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_H36B}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_JM9130013}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_COH1}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M781}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M732}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
Consensus	*****	*****	*****
	51		100
msa442834.2{248_090}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS
msa442834.2{248_1169NT}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_18RS21}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_2603}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_A909}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_CJB110}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_H36B}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_JM9130013}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_COH1}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_M781}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
msa442834.2{248_M732}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NTRTLVITTA	SLVGGPLVGS
Consensus	*****	*****	*****	*****	*****
101					
msa442834.2{248_090}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_1169NT}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_18RS21}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_2603}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_A909}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_CJB110}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_H36B}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_JM9130013}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_COH1}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M781}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M732}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
Consensus	*****	*****	*****	*****	*****
151					
msa442834.2{248_090}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_1169NT}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_18RS21}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_2603}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_A909}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_CJB110}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_H36B}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_JM9130013}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_COH1}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M781}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M732}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
Consensus	*****	*****	*****	*****	*****
201					
msa442834.2{248_090}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_1169NT}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_18RS21}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_2603}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_A909}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_CJB110}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_H36B}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_JM9130013}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_COH1}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M781}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M732}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
Consensus	*****	*****	*****	*****	*****
251					
msa442834.2{248_090}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_1169NT}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_18RS21}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_2603}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_A909}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_CJB110}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_H36B}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_JM9130013}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_COH1}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M781}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M732}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
Consensus	*****	*****	*****	*****	*****
301					
msa442834.2{248_090}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_1169NT}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_18RS21}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_2603}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_A909}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_CJB110}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_H36B}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_JM9130013}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_COH1}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M781}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M732}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
Consensus	*****	*****	*****	*****	*****
351					
msa442834.2{248_090}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNIAINT	ISALIRIDSD
400					

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_1169NT}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_18RS21}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_2603}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_A909}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_CJB110}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_H36B}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_JM9130013}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_COH1}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M781}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M732}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
Consensus	*****	*****	*****	*****	*****
401					
msa442834.2{248_090}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_1169NT}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_18RS21}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_2603}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_A909}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_CJB110}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_H36B}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_JM9130013}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_COH1}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_M781}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
msa442834.2{248_M732}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYQ
Consensus	*****	*****	*****	*****	*****
450					
451					
msa442834.2{248_090}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_1169NT}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_18RS21}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_2603}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_A909}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_CJB110}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_H36B}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_JM9130013}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_COH1}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M781}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M732}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
Consensus	*****	*****	*****	*****	*****
500					
501					
msa442834.2{248_090}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_1169NT}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_18RS21}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_2603}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_A909}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_CJB110}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_H36B}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_JM9130013}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_COH1}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M781}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M732}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
Consensus	*****	*****	*****	*****	*****
550					
551					
msa442834.2{248_090}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_1169NT}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_18RS21}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_2603}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_A909}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_CJB110}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_H36B}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_JM9130013}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_COH1}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M781}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M732}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
Consensus	*****	*****	*****		
580					

Table 59: Comparative Sequences relating to SAG2147

SEQ ID NO. 5901

STRAIN 2603

ATGAATAAAAGAAGAAAATTATCAAAATTGAATGTAAAAAACATCATTTAGCTTATGGA
GCTATCACCTTTAGTAGCCCTTTTTTCATGTATTTGGCTGTAATGGTCATCTTTAAAAGT
TCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCCAAAAAATCA
AAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCAAAACCT
TCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAG
CAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAACAGAAAAACACC
CCTGCTACCAAGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCT
CAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACATGCAGGGGCTATTGGCTCA
GCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATT
ATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTT
TTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTTCAAGATCAAGTTAATTCAGCT
ATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTACTAG

SEQ ID NO. 5902

STRAIN JM9130013

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAA
AGCAGATAAAGTTTCGCGTAGCCAAAAAATCAAAAATGAATAAGGCAACAT
CTAAATCAAAAGTAGAAGGTGTAAACAGGCTCCAAAACCAAGTTCTCAA
TCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGC
TGTAAGAACAAGCAGTTGTAAACAGAAAAATACCCCTGCTACCAAGTCAAGCAC
AACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAG
CCGAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGTTATTGGCTC
AGCAGCAGCAGCACAAATGGCTGCTGCAACGGGAGTTCTCAGTCTACTT
GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAACGTTGCTAAT
GCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAAC
AGCTACAGTTTCAAGATCAAGTTAATCAGCTATTAAAGCTTATCGTGCTC
AAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5903

STRAIN 1169NT reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCC
AAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCT
CCAAAACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCT
AATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAAC
GAAAATACCCCTGCTACCAAGTCAGGCACAACAACCTTATGCTGTTACTGAGACAACCTTAC
AAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAAATACTGCAGGGGCG
GTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGG
GAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCT
TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTTCAAGATCAAGTT
AATTCAAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5904

STRAIN 18RS21 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTC
GCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAA
AACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTA
CAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAG
TTGTAACAGAAAAACACCCCTGCTACCAAGTCAGGCACAACAAGCTTATGCTGTTACTGAGA
CAACTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACTG
CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGT
CTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCT
CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTTCAAG
ATCAAGTTAATTCAAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5905

STRAIN 090 reverse complement

TAGCCAAAAAATCAAAAATGATTAAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAC
AGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAG
AAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTG
TAACAGAAAAACACCCCTGCTACCAAGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAA
CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACTGCAG
GGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA
CTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAG
GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTTCAAGGA

SEQ ID NO. 5906

STRAIN A909 reverse complement

AAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCA
TCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTT
ACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAAACAGAAAAACACCCCTGCTACC
AGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAG
ACAAGTGGCCAAAGTATTGAGTAATGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCA
GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGT
GAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG
ATGCCAGGTTGGGGTTCAACAGCTACAGTTTCAAGATCAAGTTAATTCAAGCTATTAAAGCT
TATCGTGCTCAAGGTTTATCA

SEQ ID NO. 5907

STRAIN CJB110 reverse complement

AATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGA

Table 59: Comparative Sequences relating to SAG2147

CATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATG
 AAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGA
 GTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAAACAGAAAAACCCCTGCTACCAAGTCAGG
 CACAACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAGACGAGTG
 GCCAAGTATTGAGTAATGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA
 TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA
 ATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAG
 GTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTG
 CTAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5908

STRAIN COH1 reverse complement

AAAAGTTTCAAGTTACTACTGAATCTTTGTCAAAGCAGATAA
 AGTTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGA
 TGTAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCA
 ATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA
 AGCAGTTGTAAACAGAAAAATACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTAC
 TGAGACAACCTTACAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAA
 TACTGCAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCC
 TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA
 TGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT
 TCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG
 TTAC

SEQ ID NO. 5909

STRAIN H36B reverse complement

AAAAGTTTCAAGTTACTACTGAATCTTTGTCAAAGC
 AGATAAAGTTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGT
 AGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAG
 TTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGT
 AGAACAAGCAGTTGTAAACAGAAAAACCCCTGCTACCAAGTCAGGCACAACAACTTATGC
 TGTACTGAGACAACCTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA
 TGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGG
 AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGT
 TGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGC
 TACAGTTTCAAGTTAATTCAGCTATTAAAGCTT

SEQ ID NO. 5910

STRAIN M732 reverse complement

AAAAGTTTCAAGTTACTACTGAATCTTTGTCAAAGCAGATAAAGTTTCGCGTAGC
 CAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGC
 TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGC
 TAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAAC
 AGAAAAATACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
 CAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGC
 GGTTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG
 GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGC
 TTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTTCAAGATCAAGT
 TAATTTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

SEQ ID NO. 5911

STRAIN M781 reverse complement

TCTTTGTCAAAGCAGATAAAGTTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACA
 TCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAA
 GCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGT
 GAAGAGGCGGCTGTAGAACAAGCAGTTGTAAACAGAAAAATACCCCTGCTACCAAGTCAGGCA
 CAACAACTTATGCTGTTACTGAGACAACCTTACAAACCTGCTCAACACCAGACAAGTGGC
 CAAGTATTGAGCAATGGAAATACTGCAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATG
 GCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAAT
 GGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGT
 TGGGGTTCAACAGCTACAGTTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCT
 CAAGGTTTATCAGCTTGGGGTTAC

PRETTY of: /biotmp/msa519780.2{*} March 10, 2003 06:25 ..

	1				50
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	atgaataaaa	gaagaaaatt	atcaaaaattg	aatgtaaaaa	aacatcattt
msa519780.2{25_H36B}	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	agcttatgga	gctatcactt	tagtagccct	tttttcatgt	attttggctg
msa519780.2{25_H36B}	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa519780.2{25_COH1}	-----	-----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_M781}	-----	-----	-----	-----tc	tttgtcaaaa
msa519780.2{25_M732}	-----	-----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_1169NT}	-----	-----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_18RS21}	-----	-----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----aatc	tttgtcaaaa
msa519780.2{2603}	taatgggtcat	ctttaaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_H36B}	-----	-----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_JM9130013}	-----	-----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
Consensus	*****	****-	-----	-----	-----
	151				200
msa519780.2{25_COH1}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_M781}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_M732}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_1169NT}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_18RS21}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_A909}	-----	-----	-----	-----A	AGGCgACATC
msa519780.2{25_090}	-----	-----tagc	caaaaaatca	aaaatgattA	AGGCgACATC
msa519780.2{25_CJB110}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{2603}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_H36B}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_JM9130013}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgaatA	AGGCaACATC
Consensus	-----	-----	-----	-----*	*****
	201				250
msa519780.2{25_COH1}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_M781}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_M732}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_1169NT}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_18RS21}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_A909}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_090}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_CJB110}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{2603}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_H36B}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcagggcat
msa519780.2{25_JM9130013}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAAC..
Consensus	*****	*****	*****	*****	-----
	251				300
msa519780.2{25_COH1}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_M781}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_M732}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_1169NT}	ctaatagaagt	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_18RS21}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_A909}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_090}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_CJB110}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{2603}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_H36B}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_JM9130013}CA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
Consensus	-----	-----**	*****	*****	*****
	301				350
msa519780.2{25_COH1}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_M781}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_M732}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_1169NT}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_18RS21}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_A909}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_090}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_CJB110}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{2603}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_H36B}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_JM9130013}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa519780.2{25_COH1}	AGAAAAaACC	CCTGCTACCA	GTCagGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_M781}	AGAAAAaACC	CCTGCTACCA	GTCagGCACA	ACAAaCTTAT	GCTGTTACTG

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M732}	AGAAAAAtACC	CCTGCTACCA	GTCAGGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_1169NT}	AGAAAAAtACC	CCTGCTACCA	GTCAGGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_18RS21}	AGAAAAcACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_A909}	AGAAAAcACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_090}	AGAAAAcACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_CJB110}	AGAAAAcACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{2603}	AGAAAAcACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_H36B}	AGAAAAcACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_JM9130013}	AGAAAAAtACC	CCTGCTACCA	GTCaAGCACA	ACAAGCTTAT	GCTGTTACTG
Consensus	*****-***	*****	****-*****	*****	*****
msa519780.2{25_COH1}	AGACAACTTA	cAaACCTGCT	CAACACCAGa	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M781}	AGACAACTTA	cAaACCTGCT	CAACACCAGa	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M732}	AGACAACTTA	cAaACCTGCT	CAACACCAGa	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_1169NT}	AGACAACTTA	cAaACCTGCT	CAACACCAGa	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_18RS21}	AGACAACTTA	tAgACCTGCT	CAACACCAGa	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_A909}	AGACAACTTA	tAgACCTGCT	CAACACCAGa	CaAGTGGCCA	AGTATTGAGt
msa519780.2{25_090}	AGACAACTTA	tAgACCTGCT	CAACACCAGa	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_CJB110}	AGACAACTTA	tAgACCTGCT	CAACACCAGa	CgAGTGGCCA	AGTATTGAGt
msa519780.2{2603}	AGACAACTTA	tAgACCTGCT	CAACACCAGa	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_H36B}	AGACAACTTA	tAgACCTGCT	CAACACCAGa	CaAGTGGCCA	AGTATTGAGt
msa519780.2{25_JM9130013}	AGACAACTTA	tAgACCTGCT	CAACACCAGc	CgAGTGGCCA	AGTATTGAGc
Consensus	*****	-*-*****	*****	*-*****	*****
msa519780.2{25_COH1}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTCt	GctGctGCAG	CACAAATGGC
msa519780.2{25_M781}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTCt	GctGctGCAG	CACAAATGGC
msa519780.2{25_M732}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTCt	GctGctGCAG	CACAAATGGC
msa519780.2{25_1169NT}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTCt	GctGctGCAG	CACAAATGGC
msa519780.2{25_18RS21}	AATGGAAATA	CTGCAGGGGc	taTtGGcTCa	GcAGctGCAG	CACAAATGGC
msa519780.2{25_A909}	AATGGAAATA	CTGCAGGGGc	taTtGGcTCa	GcAGctGCAG	CACAAATGGC
msa519780.2{25_090}	AATGGAAATA	CTGCAGGGGc	taTtGGcTCa	GcAGctGCAG	CACAAATGGC
msa519780.2{25_CJB110}	AATGGAAATA	CTGCAGGGGc	taTtGGcTCa	GcAGctGCAG	CACAAATGGC
msa519780.2{2603}	AATGGAAATA	CTGCAGGGGc	taTtGGcTCa	GcAGctGCAG	CACAAATGGC
msa519780.2{25_H36B}	AATGGAAATA	CTGCAGGGGc	taTtGGcTCa	GcAGctGCAG	CACAAATGGC
msa519780.2{25_JM9130013}	AATGGAAATA	CTGCAGGGGt	taTtGGcTCa	GcAGcAGCAG	CACAAATGGC
Consensus	*****	*****	-*-*-*-*	*-*-*-*	*****
msa519780.2{25_COH1}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M781}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M732}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_1169NT}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_18RS21}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_A909}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_090}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_CJB110}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{2603}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_H36B}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_JM9130013}	TGCTGCAACg	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M781}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M732}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_1169NT}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_18RS21}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_A909}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_090}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_CJB110}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{2603}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_H36B}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_JM9130013}	AATCAAATGG	TAATCCTAAc	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M781}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M732}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_1169NT}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_18RS21}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_A909}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGaAtcaagt
msa519780.2{25_090}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgA-----
msa519780.2{25_CJB110}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{2603}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_H36B}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_JM9130013}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
Consensus	*****	*****	*****	*****	*-*****
msa519780.2{25_COH1}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M781}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_M732}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_1169NT}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_18RS21}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_A909}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	~~~~~
msa519780.2{25_090}	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
msa519780.2{25_CJB110}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{2603}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_H36B}	taattcagct	attaaagctt	~~~~~	~~~~~	~~~~~
msa519780.2{25_JM9130013}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
Consensus	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~

	701
msa519780.2{25_COH1}	ac---
msa519780.2{25_M781}	ac---
msa519780.2{25_M732}	a----
msa519780.2{25_1169NT}	ac---
msa519780.2{25_18RS21}	ac---
msa519780.2{25_A909}	~~~~~
msa519780.2{25_090}	~~~~~
msa519780.2{25_CJB110}	ac---
msa519780.2{2603}	actag
msa519780.2{25_H36B}	~~~~~
msa519780.2{25_JM9130013}	ac---
Consensus	---**

SEQ ID NO. 5912

STRAIN 2603 frame: 1

MNKRRLSKLNVKHHLAYGAILVALFSCILAVMVIKSSQVTTESLSKADKVRVAKKS
 KMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENT
 PATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI
 IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQGLSAWGY

SEQ ID NO. 5913

STRAIN 1169NT frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPAT SQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSAWGY

SEQ ID NO. 5914

STRAIN 18RS21 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPAT SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSAWGY

SEQ ID NO. 5915

STRAIN 2603 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPAT SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSAWGY

SEQ ID NO. 5916

STRAIN 090 frame: 3

AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVV
 TENTPAT SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQST
 WEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQ

SEQ ID NO. 5917

STRAIN A909 frame: 1

KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENTPAT
 SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI IAR
 ESNNGNPNVANASGASGLFQTMPGWGSTATVQNVNSAIKAYRAQGLS

SEQ ID NO. 5918

STRAIN CJB110 frame: 3

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
 EEAAVEQAVVTENTPAT SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQM
 AATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
 QGLSAWGY

SEQ ID NO. 5919

STRAIN COH1 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPAT SQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSAWGY

SEQ ID NO. 5920

STRAIN H36B frame: 1

Table 59: Comparative Sequences relating to SAG2147

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPATSAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKA

SEQ ID NO. 5921

STRAIN M732 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPATSAQQAYAVTETTYKPAQHQTSGQVLSNGNTAGAV
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSAWG

SEQ ID NO. 5922

STRAIN M781 frame: 4

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
 EEAQVEQAVVTENTPATSAQQAYAVTETTYKPAQHQTSGQVLSNGNTAGAVGSAAAAQMA
 AATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
 QGLSAWGY

SEQ ID NO. 5923

STRAIN JM9130013 frame: 1

KSSQVTTESLSKADKVRVAKKSKMNKATSKSKVEGVKQAPKPSQSTEANSQQQVTASEE
 AAVEQAVVTENTPATSAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGVIGSAAAAQMAA
 ATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQ
 LSAWGY

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa519418.2{*} March 10, 2003 06:15 ..

	1				50
msa519418.2{25_090}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_H36B}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_COH1}	-----	-----	-----	-----	-----SLSK
msa519418.2{25_M781}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_1169NT}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M732}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_18RS21}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_CJB110}	-----	-----	-----	-----	-----SLSK
msa519418.2{25_2603}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{2603}	mnkrrklsl	nvkhhlayg	aitlvalfsc	ilavmvifks	SQVTTESLSK
msa519418.2{25_A909}	-----	-----	-----	-----	-----
msa519418.2{25_JM9130013}	-----	-----	-----	-----KS	SQVTTESLSK
Consensus	*****	*****	*****	*****	*****
	51				100
msa519418.2{25_090}	-----akks	kmiKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_H36B}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_COH1}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_M781}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_1169NT}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasnevpks	SSQSTEANSQ
msa519418.2{25_M732}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_18RS21}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_CJB110}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_2603}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{2603}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_A909}	-----	---KATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_JM9130013}	ADKVRVakks	kmnKATSKSK	VEGVKQAPKP	SSQSTEANSQ
Consensus	*****	-----	***-----	-----	*****
	101				150
msa519418.2{25_090}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_H36B}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_COH1}	QQVTASEEAA	VEQAVVTENT	PATSAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_M781}	QQVTASEEAA	VEQAVVTENT	PATSAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_1169NT}	QQVTASEEAA	VEQAVVTENT	PATSAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_M732}	QQVTASEEAA	VEQAVVTENT	PATSAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_18RS21}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_CJB110}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_2603}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{2603}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_A909}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_JM9130013}	QQVTASEEAA	VEQAVVTENT	PATSAQQaY	AVTETTYrPA	QHQtSGQVLS
Consensus	*****	*****	*****	*****	*****
	151				200
msa519418.2{25_090}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_H36B}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_COH1}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_M781}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_1169NT}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_M732}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_18RS21}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_CJB110}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL

Table 59: Comparative Sequences relating to SAG2147

msa519418.2{25_2603}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{2603}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_A909}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_JM9130013}	NGNTAGviGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
Consensus	*****-***	*****	*****	*****	*****
		201		234	
msa519418.2{25_090}	FQTMPGWGST	ATVQ-----	-----	----	
msa519418.2{25_H36B}	FQTMPGWGST	ATVQDQVNSA	IKA-----	----	
msa519418.2{25_COH1}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M781}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_1169NT}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M732}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWG~	
msa519418.2{25_18RS21}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_CJB110}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_A909}	FQTMPGWGST	ATVQnQVNSA	IKAYRAQGLS	----	
msa519418.2{25_JM9130013}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
Consensus	*****	*****	*****	****	

Table 60: Comparative Sequences relating to SAG1945

SEQ ID NO. 6001

STRAIN 2603

ATGAAAGAAAAACAGTCGAAAAGGCTTATTTATATACTACTGGTTGTTTCCATTATTTTT
ATAAGTGTTTTTACATACAGTATTAGCCAGCCTTCTAAACTACTTCCACCAAAGAATTA
GTTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAA
AAATACGGTATAAAAGTTAAGCTTATTCAGGTGGGACAGGGCAACTAATAGATAGATTA
AGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATATACGCAATTT
GAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATGTTCTACTGTTATTCCA
GACTATATCCATCCAAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATT
GTAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCT
TCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCTCTAGTGCTTTCTCACA
CTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACATGTT
AAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAA
TCAGTTGCAGAAGGAAAAATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTG
CAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCA
TCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAAT
TTTATGCTTTCTTTAGATGTTCAAAATGCCCTTTGGGCAGTCAACGAGTAACCGACCTATT
CGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAA
GAAGATTATCGCTATGTCACATAAGGGCCAAATCCTTAAAACCTATAATCGTATT
CGTAGAAATGCTGAT

SEQ ID NO. 6002

STRAIN 090

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGT
CCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAA
ATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAG
ATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTTTGGA
GGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGT
ATCAAAGAATGTTCTACTGTTTATTCCAGACTATATCCATCCAAGTGATA
CGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAA
TTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTC
CTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCTCTAGTGCTT
TCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCA
AAAGCGTGGAACCTATGTTAAAAGCTACAACATAATATTAAATGCTATCAA
ATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGA
TTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAGTGGT
GCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATC
TTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTAT
TTATTAATTTTATGCTTCTTTAGATGTTCAAAATGCCCTTTGGGCAGTCA
ACGAGTAACCGACCTATTTCGTAAAGATGCCCAAACGAGTAATGGCATGAA
AGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCATA
AGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTTCGTAGAAATGCT
GAT

SEQ ID NO. 6003

STRAIN A909

CAGCCTTCTAAACTACTTCCACCAAAGAATTAG
TTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCT
TTTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGG
TCAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATA
TTTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTT
GAGTCTTACGTATCAAAGAATATTCTACTGTTATTCCAGATTATATCCA
TCCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTG
TAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTA
TTACAGCCTTCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTC
CTCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTT
ACACCAATCCAAAAGCGTGGAACCTATGTTAAAAGCTACAACATAATATT
AATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGA
AGGAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGC
AAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT
TTTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGA
AGCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCT
TTGGGCAGTCAACGAGTAACCGACCTATTTCGTAAAGATGCCCAAACGAGT
AATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG
CTATGTCATAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTTC
GTAGAAATGCTGAT

SEQ ID NO. 6004

STRAIN H36B

TAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG
CCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATACGGTATAAAA
GTTAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAAGTAA
GGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATATACGC
AATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATATT
CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA
TACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAGTTAAGGGAC
TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCTTAAAAGGTAAA
ATTGCCTTTGCAGATCCGAATACTTCTCTAGTGCTTTCTCACAACCTCAC
TAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAAC
ATGTTAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCT
TCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGTGGGGTTGAC
TTACGAAGACCCTAGTGTCAATTTGCAAAAAGTGGTGCCAATGTTTCTA
TTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCGGTTGCAATT

Table 60: Comparative Sequences relating to SAG1945

ATAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAATTTTAT
GCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAGTAACCGAC
CTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT
ATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCATAAGGGCCA
AATCCTTAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6005**STRAIN 18RS21**

CAGCCTTCTAAACTACTTCCACCAAAAAGAATTAGTTATTCTAAGTCCAAA
TAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATACG
GTATAAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGA
TTAAGTAAGGAGGGTAAGCAGTTGAAGGCGATATTTCTTTGGAGGAAA
TTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAA
AGAATGTTTCATACTGTTATTCCAGACTATATCCATCCAAGTGATACGGCG
ACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAGC
TAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTAA
AAGGTAAAATTGCCTTTGTCAGATCCGAATACTTCTCTAGTGCTTTCTCA
CAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGC
GTGGAACATATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCTT
CTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGTG
GGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGTGCCAA
TGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCGG
TTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATT
AATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAG
TAACCGACCTATTTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTT
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCAT
AAGGGCCAAATCCTTAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6006**STRAIN M732**

CAGCCTTCTAAACTACTTCCACCAAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATAT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTTCATACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAGGTAAAATTGCCTTTGTCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACATATGTTAAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
GGAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTTCGTAAAGATGCCCAAACAAGTA
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
TATGTCACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCG
TAGAAATGCTGAT

SEQ ID NO. 6007**STRAIN COH1**

CAGCCTTCTAAACTACTTCCACCAAAAAGAATTAGT
ATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTT
TGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGC
AACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATT
TTCCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGA
GTCTTACGTATCAAAGAATGTTTCATACTGTTATTCCAGACTATATCCATC
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATT
ACAGCCTTCCTTAAAGGTAAAATTGCCTTTGTCAGATCCGAATACTTCTC
CTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTAC
ACCAATCCAAAAGCGTGGAACATATGTTAAAAAGCTACAACATAATATTA
TGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
GAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAA
AAAAGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG
CAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTT
GGGCAGTCAACGAGTAACCGACCTATTTCGTAAAGATGCCCAAACAAGTAA
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT
ATGTCACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCGT
AGAAATGCTGAT

SEQ ID NO. 6008**STRAIN M781**

CAGCCTTCTAAACTACTTCCACCAAAAAGAATTAGTTATT
CTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGA
GGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC
TAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTC
TTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTC
TTACGTATCAAAGAATGTTTCATACTGTTATTCCAGACTATATCCATCCGA
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT

Table 60: Comparative Sequences relating to SAG1945

AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA
GCCTTCCTTAAAAGGTAAAATTGCCCTTTCAGATCCGAATACTTCCTCTA
GTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACC
AATCCAAAAGCGTGGAACCTATGTTAAAAAGCTACAACATAATATTAATGC
TATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAA
AAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAA
AGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTGTGT
CCCATCTTCGGTTGCAATTTATAAAGAATGCTCCTTCTATGAAAGAAGCAA
AGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGG
CAGTCAACGAGTAACCGACCTATTGTAAGATGCCCAAACAAGTAATGG
CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
TCACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTGCTAGA
AATGCTGAT

SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT
AAGTCCAAATAGTCAAGCCATTTAACAGGAACGATTCCAGCTTTTGAGg
AAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
ATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTT
TGGAGGAAATTTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTT
ACGTATCAAAGAATGTTCACTGTTATTCCAGACTATATCCATCCAAGT
GATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAA
CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGC
CTTCTTAAAAGGTAAAATTGCCCTTTCAGATCCGAATACTTCCTCTAGT
GCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA
TCCAAAAGCGTGGAACCTATGTTAAAAAGCTACAACATAATATTAATGCTA
TCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAAGGAAAA
ATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAG
TGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCC
CATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAG
TTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCA
GTCAACGAGTAACCGACCTATTGTAAGATGCCCAAACGAGTAATGGCA
TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC
ACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTGCTAGAAA
TGCTGAT

SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC
GGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
ATTAAGTAAGGAGGGTAAGCATTGGAAGGCGGATATTTCTTGGAGGAA
ATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCA
AAGAATGTTCACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC
GACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAG
CTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTA
AAAGGTAAAATTGCCCTTTCAGATCCGAATACTTCCTCTAGTGCTTCTC
ACAACCTACCAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAAG
CGTGGAACCTATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCT
TCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGT
GGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGTGCCA
ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCG
GTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTAT
TAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGA
GTAACCGACCTATTGTAAGATGCCCAAACGAGTAATGGCATGAAAGCT
TTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCA
TAAGGGCCAAATCCTTAAACCTATAATCGTATTGCTAGAAATGCTGAT

SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG
AGTCTTACGTATCAAAGAATGTTCACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAGGTAAAATTGCCCTTTCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACCTACCAATATACTCTTGGCAAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACCTATGTTAAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAA
GGCAAAATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAATGTTTCTATTGTATCCGACAGAAGGGACAGTTT
TTGTCCCCTCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTGTAAGATGCCCAAACGAGTA
ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC
TATGTCACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTGCT
TAGAAATGCTGAT

PRETTY of: /biotmp/msa523010.2(*) April 28, 2003 08:55 ..

Table 60: Comparative Sequences relating to SAG1945

	1				50
msa523010.2{263_COH1}	-----	-----	-----	-----	-----
msa523010.2{263_M732}	-----	-----	-----	-----	-----
msa523010.2{263_M781}	-----	-----	-----	-----	-----
msa523010.2{263_A909}	-----	-----	-----	-----	-----
msa523010.2{263_H36B}	-----	-----	-----	-----	-----
msa523010.2{263_090}	-----	-----	-----	-----	-----
msa523010.2{263_18RS21}	-----	-----	-----	-----	-----
msa523010.2{263_2603}	atgaaagaaa	aacagtcgaa	aaggcttatt	tatatactac	tggttggttc
msa523010.2{263_CJB110}	-----	-----	-----	-----	-----
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa523010.2{263_COH1}	-----	-----	-----	-----cag	ccttctaacc
msa523010.2{263_M732}	-----	-----	-----	-----cag	ccttctaacc
msa523010.2{263_M781}	-----	-----	-----	-----cag	ccttctaacc
msa523010.2{263_A909}	-----	-----	-----	-----cag	ccttctaacc
msa523010.2{263_H36B}	-----	-----	-----	-----	-----taaac
msa523010.2{263_090}	-----	-----	-----	-----cag	ccttctaacc
msa523010.2{263_18RS21}	-----	-----	-----	-----cag	ccttctaacc
msa523010.2{263_2603}	cattattttt	ataagtgtt	ttacatacag	tatttagccag	ccttctaacc
msa523010.2{263_CJB110}	-----	-----	-----	-----cag	ccttttaaac
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----cag	ccttctaacc
Consensus	*****	*****	*****	*****	-----
	101				150
msa523010.2{263_COH1}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M732}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M781}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_A909}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_H36B}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_090}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_18RS21}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_2603}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_CJB110}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_1169NT}	-----	-----	-----	-----ATAG	TCAAGCCATT
msa523010.2{263_JM91130013}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
Consensus	-----	-----	-----	-----****	*****
	151				200
msa523010.2{263_COH1}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M732}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M781}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_A909}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_H36B}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_090}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_18RS21}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_2603}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_CJB110}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_1169NT}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_JM91130013}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa523010.2{263_COH1}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M732}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M781}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_A909}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_H36B}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_090}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_18RS21}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_2603}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_CJB110}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_1169NT}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_JM91130013}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
Consensus	*****	*****	*-*****	*****	*****
	251				300
msa523010.2{263_COH1}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M732}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M781}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_A909}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_H36B}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_090}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_18RS21}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_2603}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_CJB110}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_1169NT}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_JM91130013}	GTAAGCagTT	GAAGGCGGAT	gTTTTCTTTG	GAGGAAATTA	TACGCAATTT
Consensus	*****-*	*****	-*****	*****	*****

Table 60: Comparative Sequences relating to SAG1945

	301				350
msa523010.2{263_COH1}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M732}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M781}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_A909}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_H36B}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_090}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_18RS21}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_2603}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_CJB110}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_1169NT}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_JM91130013}	GAAAGTCATA	AGGCATTGTT	TGAGTCCTTAC	GTATCAAAGA	ATgTTCATAC
Consensus	*****	*****	*****	*****	**-*****
	351				400
msa523010.2{263_COH1}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M732}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M781}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_A909}	TGTTATTCCA	GAtTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_H36B}	TGTTATTCCA	GAtTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_090}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_18RS21}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_2603}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_CJB110}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_1169NT}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_JM91130013}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
Consensus	*****	**-*****	****-*****	*****	*****
	401				450
msa523010.2{263_COH1}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M732}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M781}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_A909}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_H36B}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGtTAA	GGGACTTACC
msa523010.2{263_090}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_18RS21}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_2603}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_CJB110}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_1169NT}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_JM91130013}	TAAATGGGAG	TGTCCTTGATT	GTAAATAACG	AATTAGcTAA	GGGACTTACC
Consensus	*****	*****	*****	*****-***	*****
	451				500
msa523010.2{263_COH1}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_M732}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_M781}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_A909}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_H36B}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_090}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_18RS21}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_2603}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_CJB110}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_1169NT}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
msa523010.2{263_JM91130013}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAAAATTGC
Consensus	*****	*****	*****	*****	*****
	501				550
msa523010.2{263_COH1}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_M732}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_M781}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_A909}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_H36B}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_090}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_18RS21}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_2603}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_CJB110}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACTAATA
msa523010.2{263_1169NT}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACcAATA
msa523010.2{263_JM91130013}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCACcAATA
Consensus	*****	*****	*****	*****	*****-****
	551				600
msa523010.2{263_COH1}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_M732}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_M781}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_A909}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_H36B}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_090}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_18RS21}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_2603}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_CJB110}	TACTCTTGGC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_1169NT}	TACTCTTGGC	aAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT
msa523010.2{263_JM91130013}	TACTCTTGGC	aAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACATATGTT

Table 60: Comparative Sequences relating to SAG1945

Consensus	*****	-*****	*****	*****	*****
	601				650
msa523010.2{263_COH1}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M732}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M781}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_A909}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_H36B}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_090}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_18RS21}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_2603}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_CJB110}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_1169NT}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_JM91130013}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa523010.2{263_COH1}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M732}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M781}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_A909}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_H36B}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_090}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	cTGACTTACG
msa523010.2{263_18RS21}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	cTGACTTACG
msa523010.2{263_2603}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	cTGACTTACG
msa523010.2{263_CJB110}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	cTGACTTACG
msa523010.2{263_1169NT}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_JM91130013}	AGTTTATCAA	TCAGTTGCAG	AAGGcAAAAT	GATTGTGGGG	cTGACTTACG
Consensus	*****	*****	*****	*****	-*****
	701				750
msa523010.2{263_COH1}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M732}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M781}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_A909}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_H36B}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_090}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_18RS21}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_2603}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_CJB110}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_1169NT}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_JM91130013}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTg
Consensus	*****	*****	*****	*****	*****-
	751				800
msa523010.2{263_COH1}	TACCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M732}	TACCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M781}	TACCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_A909}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_H36B}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_090}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_18RS21}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_2603}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_CJB110}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_1169NT}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_JM91130013}	TATCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
Consensus	**--*****	*****	*****	*****	*****
	801				850
msa523010.2{263_COH1}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M732}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M781}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_A909}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_H36B}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_090}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_18RS21}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_2603}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_CJB110}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_1169NT}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_JM91130013}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
Consensus	*****	*****	*****	*****	*****
	851				900
msa523010.2{263_COH1}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M732}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M781}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_A909}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_H36B}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_090}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_18RS21}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_2603}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_CJB110}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_1169NT}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT

Table 60: Comparative Sequences relating to SAG1945

msa523010.2{263_JM91130013}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
Consensus	*****	*****	*****	*****	*****
	901				950
msa523010.2{263_COH1}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M732}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M781}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_A909}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_H36B}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_090}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_18RS21}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_2603}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_CJB110}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_1169NT}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_JM91130013}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
Consensus	*****	*****-*	*****	*****	*****-*
	951				1000
msa523010.2{263_COH1}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	aGCCAAATCC
msa523010.2{263_M732}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	aGCCAAATCC
msa523010.2{263_M781}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	aGCCAAATCC
msa523010.2{263_A909}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_H36B}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_090}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_18RS21}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_2603}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_CJB110}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_1169NT}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_JM91130013}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
Consensus	*****	*****	*****	*****	-*****
	1001				1035
msa523010.2{263_COH1}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M732}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M781}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_A909}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_H36B}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_090}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_18RS21}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_2603}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_CJB110}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_1169NT}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_JM91130013}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
Consensus	*****	*****-*	*****	*****	

SEQ ID NO. 6012

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVVSIIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTPAFEE
 KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP
 DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ
 LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEKMIIVGLTYEDPSVNL
 QKSGANVSIVYPTEGTVFVPSSVAIIKNAPSMKEAKLFINFMLSLDVQNAFGQSTSNRPI
 RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF
 FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGLTIK
 SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINAIKS
 SSSSEVYQSVAEKMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNAPSM
 KEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQ
 ILKTYNRIRRNAD

SEQ ID NO. 6016

Table 60: Comparative Sequences relating to SAG1945

STRAIN 18RS21 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLS LQVNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6017

STRAIN M732 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLS LQVNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6018

STRAIN COH1 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLS LQVNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6019

STRAIN M781 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLS LQVNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6020

STRAIN CJB110 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLS LQVNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6021

STRAIN 1169NT frame: 3

SQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL
 FESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKI
 AFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINAIKSSSSSEVYQSVAEKGM
 IVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNAPSMKEAKLFINFMLS LQ
 VNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6022

STRAIN JM91130013 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DVFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAOWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSSVAIIKNA
 PSMKEAKLFINFMLS LQVNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKEDYRYVTKH
 KGQILKTYNRIRRNAD

PRETTY of: /biotmp/msa523117.2{*} April 28, 2003 08:56 ..

	1				50
msa523117.2{263_COH1}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_M732}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_M781}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_1169NT}	-----		-----SQAI		
msa523117.2{263_CJB110}	-----q	pfklppkel	vilspnSQAI		
msa523117.2{263_090}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_18RS21}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_2603}	mkekqskrli	yillvvsliif	isvftysisq	psklppkel	vilspnSQAI
msa523117.2{263_A909}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_JM91130013}	-----q	psklppkel	vilspnSQAI		
msa523117.2{263_H36B}	-----	--klppkel	vilspnSQAI		
Consensus	*****	*****	*****	-----	*****
	51				100
msa523117.2{263_COH1}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_M732}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_M781}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_1169NT}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKhLKAD	iFFGGNYTQF

Table 60: Comparative Sequences relating to SAG1945

msa523117.2{263_CJB110}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_090}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_18RS21}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_2603}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_A909}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_JM91130013}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	vFFGGNYTQF
msa523117.2{263_H36B}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
Consensus	*****	*****	*****	*****	*****
101					
msa523117.2{263_COH1}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M732}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M781}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_1169NT}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_CJB110}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_090}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_18RS21}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_2603}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_A909}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_JM91130013}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_H36B}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELvKGLT
Consensus	*****	*****	*****	*****	*****
151					
msa523117.2{263_COH1}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M732}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M781}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_1169NT}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_CJB110}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_090}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_18RS21}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_2603}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_A909}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_JM91130013}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_H36B}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
Consensus	*****	*****	*****	*****	*****
201					
msa523117.2{263_COH1}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_M732}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_M781}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_1169NT}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_CJB110}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_090}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_18RS21}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_2603}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_A909}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_JM91130013}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
msa523117.2{263_H36B}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTYEDPSVNL	QKSGANVSIV
Consensus	*****	*****	*****	*****	*****
251					
msa523117.2{263_COH1}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M732}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M781}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_1169NT}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_CJB110}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_090}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_18RS21}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_2603}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_A909}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_JM91130013}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_H36B}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
Consensus	*****	*****	*****	*****	*****
301					
msa523117.2{263_COH1}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M732}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M781}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_1169NT}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_CJB110}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_090}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_18RS21}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_2603}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_A909}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_JM91130013}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_H36B}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
Consensus	*****	*****	*****	*****	*****
345					

Table 61: Comparative Sequences relating to SAG1030

SEQ ID NO. 6101

STRAIN 2603

ATGGTAAAGTTAGTGTAAAGTTCTGTAGGAACTCAAGCATCAACAGTAGCTATTTCTATG
 TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT
 CCGATGCTTCAAGGAATGATTCTTTTCTGAAACATTGAGTGAGAAATGTACAGAATTA
 CAAACCTTATATGTCTCAATTTGTGGTGTATGAGGATTTAGACTCTGTCTTTTGAATCA
 AAATTAGCAAGTGATAGGGCATCATTAAGATTGCTGAAGCACTTTTAGAGCATCTTAAC
 GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAATAAATTA
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTTAACGCCCCAT
 TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG
 GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAACCGGAGCTTTTGAAAACCAACA
 TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCC
 AAAGCTGAAGAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
 AATACTACTAAAAAAGTAATGTTTTCAGTTGATAAAAAGAAATTAATAAAGCGGCTAAT
 GAAGCGTATAAATTAGGAGAAATTAATAAAGATACCTATGAATCAATTATCAGTGGTTTA
 AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT
 CGGCTATTGATG

SEQ ID NO. 6102

STRAIN 090

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
 AACGTTAACTCCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGA
 GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGTAT
 GAGGATTTAGACTCTGTCTGTTTGAATCAAAATTAGCAAGTGATAGGGC
 ATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCAG
 AACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAATAAATTA
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATT
 TAACGCCCCATTAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
 CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT
 AGTAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGAC
 AAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAAGCTGAAG
 AACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
 AATACTACTAAAAAAGTAATGTTTTCAGTTGATAAAAAGAAATTAATAAA
 AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAATAAAGATACCTATG
 AATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG
 GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103

STRAIN 18RS21

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
 TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG
 GAACGTTAACTCCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTG
 AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGA
 TGAGGATTTAGACTCTGTCTGTTTGAATCAAAATTAGCAAGTGATAGGG
 CATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCA
 GAACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAATAAATTA
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT
 TTAACGCCCCATTAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCA
 ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA
 TAGTAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGA
 CAAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAAGCTGAA
 GAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGA
 AATACTACTAAAAAAGTAATGTTTTCAGTTGATAAAAAGAAATTAATAA
 AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAATAAAGATACCTAT
 GAATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGA
 GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

PRETTY of: /biotmp/msa185066.2{*} May 13, 2003 07:01 ..

	1		50
msa185066.2{270_090}	-----	-----	-----
msa185066.2{270_18RS21}	-----	-----	-----
msa185066.2{270_2603}	atggtaaaag	ttagtgtaag	ttctgtagga actcaagcat caacagtagc
Consensus	*****	*****	*****
	51		100
msa185066.2{270_090}	-----	-----TT	AAATGATGCA ATAACAAAAC
msa185066.2{270_18RS21}	-----	-----TT	AAATGATGCA ATAACAAAAC
msa185066.2{270_2603}	tatttctatg	ttagtgctg	tatcggtt AAATGATGCA ATAACAAAAC
Consensus	*****	*****	*****
	101		150
msa185066.2{270_090}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC AAGGGACTGC TTATTCAAAT
msa185066.2{270_18RS21}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC AAGGGACTGC TTATTCAAAT
msa185066.2{270_2603}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC AAGGGACTGC TTATTCAAAT
Consensus	*****	*****	*****
	151		200
msa185066.2{270_090}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT CCGATGCTTC AAGGAATGAT
msa185066.2{270_18RS21}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT CCGATGCTTC AAGGAATGAT
msa185066.2{270_2603}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT CCGATGCTTC AAGGAATGAT

Table 61: Comparative Sequences relating to SAG1030

Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	201				250
msa185066.2{270_18RS21}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_2603}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	251				300
msa185066.2{270_18RS21}	ATGTCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_2603}	ATGTCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	301				350
msa185066.2{270_18RS21}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACTTTTAGA
msa185066.2{270_2603}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACTTTTAGA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	351				400
msa185066.2{270_18RS21}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_2603}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	401				450
msa185066.2{270_18RS21}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAAATCTAA	TCAAAAGAAA
msa185066.2{270_2603}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAAATCTAA	TCAAAAGAAA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	451				500
msa185066.2{270_18RS21}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_2603}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	501				550
msa185066.2{270_18RS21}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_2603}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	551				600
msa185066.2{270_18RS21}	CAGGATTTTC	TGGATATAAT	AGTAAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_2603}	CAGGATTTTC	TGGATATAAT	AGTAAAACCG	GAGCTTTTGG	AAAACCAACA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	601				650
msa185066.2{270_18RS21}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_2603}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	651				700
msa185066.2{270_18RS21}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_2603}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	701				750
msa185066.2{270_18RS21}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_2603}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	751				800
msa185066.2{270_18RS21}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_2603}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	801				850
msa185066.2{270_18RS21}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_2603}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	851				900
msa185066.2{270_18RS21}	CGGCTGCCTT	ACTTAAAGAG	GTAAGCTAAAT	CAAAATTGAC	TGACACAGCT
msa185066.2{270_18RS21}	CGGCTGCCTT	ACTTAAAGAG	GTAAGCTAAAT	CAAAATTGAC	TGACACAGCT

Table 61: Comparative Sequences relating to SAG1030

msa185066.2{270_2603}	CGGCTGCCTT	ACTTAAAGAG	G TAGCTAAAT	CAAAATTGAC	TGACACAGCT
Consensus	*****	*****	*****	*****	*****
msa185066.2{270_090}	CGGCTATTGA	901	912	TG	
msa185066.2{270_18RS21}	CGGCTATTGA			TG	
msa185066.2{270_2603}	CGGCTATTGA			TG	
Consensus	*****	**			
SEQ ID NO. 6104					
STRAIN 2603 frame: 1					
MVKVSVSSVGTQASTVAISMFSRVSA LNDAITKLSSFAEAATLQGTAYSN AKSYATGTLT					
PMLQGMILFSETLSEKCTELQTLVSI CGDEDLDSVVLESKLASDRASLKIAEALLEHLN					
DDPEPSKSAISSTKSNIKKLKKRIKSNQKKLDNLNEFNHSA TVFADISNAQSTVNQALA					
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE					
NTTKKSNVSV DKKLIKAANEAYKLGEIKDYESIIISGLSNASAALLKEVAKSKLTDTA					
RLLM					
SEQ ID NO. 6105					
STRAIN 090 frame: 1					
LNDAITKLSSFAEAATLQGTAYSN AKSYATGTLTPMLQGMILFSETLSEKCTELQTLVSI					
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS					
NQKKLDNLNEFNHSA TVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW					
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTTKKNVSV DKKLIKAANEAYKLG					
EIKKDTYESIIISGLSNASAALLKEVAKSKLTD TARLLM					
SEQ ID NO. 6106					
STRAIN 18RS21 frame: 1					
LNDAITKLSSFAEAATLQGTAYSN AKSYATGTLTPMLQGMILFSETLSEKCTELQTLVSI					
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS					
NQKKLDNLNEFNHSA TVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW					
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTTKKNVSV DKKLIKAANEAYKLG					
EIKKDTYESIIISGLSNASAALLKEVAKSKLTD TARLLM					
PRETTY of: /biotmp/msa185181.2{*} May 13, 2003 07:03 ..					
msa185181.2{270_090}	1			50	
msa185181.2{270_18RS21}	-----	-----	-----LNDA	ITKLSSFAEA	ATLQGTAYSN
msa185181.2{270_2603}	mvkvs svsg	tqastvaism	fsrvsa LNDA	ITKLSSFAEA	ATLQGTAYSN
Consensus	*****	*****	*****	*****	*****
msa185181.2{270_090}	51			100	
msa185181.2{270_18RS21}	AKSYATGTLT	PMLQGMILFS	ETLSEKCTEL	QTLVVSICGD	EDLDSVVLES
msa185181.2{270_2603}	AKSYATGTLT	PMLQGMILFS	ETLSEKCTEL	QTLVVSICGD	EDLDSVVLES
Consensus	*****	*****	*****	*****	*****
msa185181.2{270_090}	101			150	
msa185181.2{270_18RS21}	KLASDRASLK	IAEALLEHLN	DDPEPSKSAI	SSTKSNIKKL	KKRIKSNQKK
msa185181.2{270_2603}	KLASDRASLK	IAEALLEHLN	DDPEPSKSAI	SSTKSNIKKL	KKRIKSNQKK
Consensus	*****	*****	*****	*****	*****
msa185181.2{270_090}	151			200	
msa185181.2{270_18RS21}	LDNLNEFNHSA	SATVFADISN	AQSTVNQALA	AVSTGFSGYN	SKTGAFGKPT
msa185181.2{270_2603}	LDNLNEFNHSA	SATVFADISN	AQSTVNQALA	AVSTGFSGYN	SKTGAFGKPT
Consensus	*****	*****	*****	*****	*****
msa185181.2{270_090}	201			250	
msa185181.2{270_18RS21}	SGQMEWTKTV	KKNWKEREDA	KAEELKSKKA	EESKKASKIE	NTTKKSNVSV
msa185181.2{270_2603}	SGQMEWTKTV	KKNWKEREDA	KAEELKSKKA	EESKKASKIE	NTTKKSNVSV
Consensus	*****	*****	*****	*****	*****
msa185181.2{270_090}	251			300	
msa185181.2{270_18RS21}	DKKKLIKAAN	EAYKLGEIKK	DTYESIIISGL	SNASAALLKE	VAKSKLTDTA
msa185181.2{270_2603}	DKKKLIKAAN	EAYKLGEIKK	DTYESIIISGL	SNASAALLKE	VAKSKLTDTA
Consensus	*****	*****	*****	*****	*****
msa185181.2{270_090}	301				
msa185181.2{270_18RS21}	RLLM				
msa185181.2{270_2603}	RLLM				
Consensus	****				

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6201

STRAIN 2603

ATGATTTTAAAAAATTTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTTACCAATTA
GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA
GCTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATAT
AGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGC
CATACATGTACGATTGAAACTGCAAACTAATTTTTAAAGAAGGTAAAACTTATCAGCA
GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGA
GACCCATAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGT
TTTAAGCCAGGGGTGAGTTTTCAATTTTACTTATCAAGATATCATCAATCATCCTGATTCT
ATTTTGTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTTCTTTAGCAGAACATTTA
GTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGAC
TTGAAACACAGGGTTTATTATTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC
ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA
TAAACATCTCCTCACAAAATTGTTTCAATTTTAAAAATACAATAGTTTFA
CTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAAATGAG
GATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGA
AACTGCAAACTAATTTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAG
CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT
GGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC
CAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCAT
CTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTGAGCTTTTCAATTT
AATTaTCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCA
TCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATTTAGTTGCAT
GTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCTAAT
GACTTGAAACACAGAGTTTATTATTAGATTACTGTAACGAAACACTTTA
TGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA
GGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA
ATGTGACGATAAACATCTCCTCACAAAATTGTTTCAATTTTAAAAATACA
ATAGTTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACT
TTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATG
TACGATTGAACTGCAAACTAATTTTTAAAGAAGGTAAAACTTATCAG
CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG
AATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTG
GTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCA
AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTGAGC
TTTCATTTTAAATTATCAAGATATCATCAATCATCCTGATTCTATTTTTGA
TGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATT
TAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTT
GTGCCTAATGACTTGAAACACAGAGTTTATTATTAGATTACTGTAACGA
AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGG
AAAATAAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA
CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
AAAAATTGTTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATT
CCAAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTA
ACTTCTGATTTTTTAAGCCATACATGTACGATTGAACTGCAAACTAAT
TTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAGCCTTTAATAAGCCTG
CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGAT
TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCG
TTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAA
CAGTAGCTTTTAAGCCAGGGGTGAGCTTTCAATTTTAAATTATCAAGATATC
ATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAA
AAATCAACTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAAC
ATTATCAAGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGA
GTTTATTATTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA
AGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAGGCGTT
TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
GAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
CAATTTTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATATAG
AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATACATGTACGATTGAACTGCAAACTAATTTTTAAAGAA
GGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG

Table 62: Comparative Sequences relating to SAG0690

GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGGTGAGTTTTTCATTTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
 TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGA
 AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
 TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6206

STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCGTT
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
 GAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
 CATTTTTTAAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATATAG
 AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
 TTTTAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTTAAAGAA
 GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
 ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG
 GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGGTGAGTTTTTCATTTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
 TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGA
 AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
 TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6207

STRAIN COH1

TTGCTGGAT
 TATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGC
 TTACGAGAAACAATATAAAAAGAAAACTGAGATACAATGTGACGATAAAC
 ATCTCCTCGCAAAAATTGTTTCATTTTTTAAAAATACAATAGTTTTACTTTT
 CCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGG
 TATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAAACTG
 CAAAATAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT
 AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA
 CCTTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATT
 CTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAA
 CAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTTCATTTTACTTA
 TCAAGATATCATCAATCATCCTGATTCTATTTTTGTATGGTTATCATCCTG
 CTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGTT
 ATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT
 GAAACACAGGGTTTATTATTATTTAGATTACTGTAACGAAACACTTTATGAGT
 GGAATCAAAAAGTTTATGATTTTCTTTGGCATTTGGAAAATAAA

SEQ ID NO. 6208

STRAIN M781

TTGCTGGA
 TTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAG
 CTTACGAGAAACAATATAAAAAGAAAACTGAGATACAATGTGACGATAAA
 CATCTCCTCGCAAAAATTGTTTCATTTTTTAAAAATACAATAGTTTTACTTT
 TCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATG
 GTATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAAACT
 GCAAACTAATTTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTT
 TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG
 ACCCTAAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAAT
 TCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGA
 ACAGGAGTTAACAGTAGGTTTTAAGCCAGGGGTGAGTTTTTCATTTTACTT
 ATCAAGATATCATCAATCATCCTGATTCTATTTTTGTATGGTTATCATCCT
 GCTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGT
 TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT
 TGAAACACAGGGTTTATTATTATTTAGATTACTGTAACGAAACACTTTATGAG
 TGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6209

STRAIN CJB110

TTGCTGGATTATCCTCGAATTAAGGC
 GTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA
 AAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCACAAAATT
 GTTCATTTTTTAAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATA
 TAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTG
 ATTTTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTTAA
 GAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT
 ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTG
 ACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTA
 ATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC
 TTTTAAAGCCAGGGGTGAGCTTTTCATTTTAAATTATCAAGATATCATCAATC
 ATCCTGATTCTATTTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAA
 CTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCA
 AGAAGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGAGTTTATT
 ATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTAT
 GATTTTCTTTGTCATTTGGAAAATAAA

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6210

STRAIN 1169NT

AATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
 AACAAATATAAAAGAAAAGTGAAGATACAATGTGACGATAAACATCTCCTC
 GCAAAAATTTGTTTCAATTTTTTAAATACAATAGTTTTACTTTTCCCTATAT
 TCCCAAATATAGAGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTT
 TAACTTCTGATTTTTTAAGCCATACATGTACGATTGAACTGCAAACTA
 ATTTTTAAAGAAGGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCC
 TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAG
 ATTACTTTGACTATGTGATGTTGAAGTGGTCAAATACCAATTCTGGTTAT
 CGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCCTCTGAACAGGAGTT
 AACAGTAGGTTTTTAAGCCAGGGTCAAGCTTTTCAATTTTACTTTATCAAGATA
 TCATCAATCATCCTGATTCTATTTTTTGATGGTTATCATCCTGCTAAAATT
 AAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCGTGTGTTATCCCAA
 ACATTATCAAGAAGATTATCAAAATCTTGTGCCAATGACTTGAAACACA
 GAGTTTATTATTTAGATTACTGTAAACGAAACACTTTATGAGTGGAATCAA
 AAAGTTTATGATTTTCTTTGTCAATTTGGAAAATAAA

SEQ ID NO. 6211

STRAIN JM9130013

ATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAATTGAGAT
 ACAATGTGACGATAAACATCTCCTCACAAAATTGTTCAATTTTTTAAAT
 ACAATAGTTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCT
 ACTTTTAAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATAC
 ATGTACGATTGAACTGCAAACTAATTTTTTAAAGAAGGTAAATCTTAT
 CAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
 AGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAA
 CTGGTCAAATACCAATTCGTTTATCGTTTAGTAATGGAAAGATTGTTAG
 GCAAAGCACCCTCTGACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGTCT
 AGCTTTTCAATTTAATTTATCAAGATATCATCAATCATCCTGATTCTATTTT
 TGATGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAAC
 ATTTAGTTGCATGTGTTATCCCAAACATTATCAAGAAGATTATCAAAGC
 CTTGTGCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAA
 CGAAACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCAAT
 TGGAAAATAAA

PRETTY of: /biotmp/msa185284.2{*} May 13, 2003 07:08 ..

	1				50
msa185284.2{271_090}	-----	-----	-----	-----	-----
msa185284.2{271_H36B}	-----	-----	-----	-----	-----
msa185284.2{271_JM9130013}	-----	-----	-----	-----	-----
msa185284.2{271_A909}	-----	-----	-----	-----	-----
msa185284.2{271_CJB110}	-----	-----	-----	-----	-----
msa185284.2{271_18RS21}	-----	-----	-----	-----	-----
msa185284.2{271_2603}	atgatttttaa	aaattttgtcg	tgccagcatat	agttttacaat	ggggagggtgt
msa185284.2{271_M732}	-----	-----	-----	-----	-----
msa185284.2{271_M781}	-----	-----	-----	-----	-----
msa185284.2{271_COH1}	-----	-----	-----	-----	-----
msa185284.2{271_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa185284.2{271_090}	-----	-----	tggt	attatcctct	aattaaggcg tttgaattgg
msa185284.2{271_H36B}	-----	-----	-----	-----	-----
msa185284.2{271_JM9130013}	-----	-----	-----	-----	-----
msa185284.2{271_A909}	-----	-----	TTGCTgg	attatcctcg	aattaaggcg tttgaattgg
msa185284.2{271_CJB110}	-----	-----	TTGCTgg	attatcctcg	aattaaggcg tttgaattgg
msa185284.2{271_18RS21}	-----	-----	TTGCTgg	attatcctcg	aattaaggcg tttgaattgg
msa185284.2{271_2603}	ttaccaatta	gctTTGCTgg	attatcctcg	aattaaggcg	tttgaattgg
msa185284.2{271_M732}	-----	-----	TTGCTgg	attatcctcg	aattaaggcg tttgaattgg
msa185284.2{271_M781}	-----	-----	TTGCTgg	attatcctcg	aattaaggcg tttgaattgg
msa185284.2{271_COH1}	-----	-----	TTGCTgg	attatcctcg	aattaaggcg tttgaattgg
msa185284.2{271_1169NT}	-----	-----	-----	aattaaggcg	tttgaattgg
Consensus	*****	*****	-----	-----	-----
	101				150
msa185284.2{271_090}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_H36B}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_JM9130013}	-----	ATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA
msa185284.2{271_A909}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_CJB110}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_18RS21}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_2603}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_M732}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_M781}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_COH1}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_1169NT}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
Consensus	-----	*****	*****	*****	*****_*
	151				200
msa185284.2{271_090}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_H36B}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_JM9130013}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_A909}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_CJB110}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_18RS21}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_2603}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M732}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M781}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_COH1}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_1169NT}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
Consensus	*****	*****	*****	-*****	*****
msa185284.2{271_090}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_H36B}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_JM9130013}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_A909}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_CJB110}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_18RS21}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_2603}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M732}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M781}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_COH1}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_1169NT}	AAAATACAAT	AGTTTTACTT	TTCCCTATAT	TCCCAAATAT	AGAGAAGCGG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_H36B}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_JM9130013}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_A909}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_CJB110}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_18RS21}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_2603}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M732}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M781}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_COH1}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_1169NT}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_H36B}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_JM9130013}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_A909}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_CJB110}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_18RS21}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_2603}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M732}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M781}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_COH1}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_1169NT}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTAAAG	AAGGTAAAT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_H36B}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_JM9130013}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_A909}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_CJB110}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_18RS21}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_2603}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M732}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M781}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_COH1}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_1169NT}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_H36B}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_JM9130013}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_A909}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_CJB110}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_18RS21}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_2603}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M732}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M781}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_COH1}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_1169NT}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
Consensus	*****	*****	*****	*****	*****

451

500

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_090}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_H36B}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_JM9130013}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_A909}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_CJB110}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_18RS21}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_2603}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_M732}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_M781}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_COH1}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_1169NT}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_H36B}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_JM9130013}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_A909}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_CJB110}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_18RS21}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_2603}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M732}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M781}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_COH1}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_1169NT}	GTTAGGCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
Consensus	*****	*****	*****	*****-*	*****
msa185284.2{271_090}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_H36B}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_JM9130013}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_A909}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_CJB110}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_18RS21}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_2603}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M732}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M781}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_COH1}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_1169NT}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
Consensus	*****-*	*****-*	*****	*****	*****
msa185284.2{271_090}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_H36B}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_JM9130013}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_A909}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_CJB110}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_18RS21}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_2603}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M732}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M781}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_COH1}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_1169NT}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
Consensus	*****	*****	*****	*****-*	*****
msa185284.2{271_090}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_H36B}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_JM9130013}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_A909}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_CJB110}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_18RS21}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_2603}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M732}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M781}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_COH1}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_1169NT}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
Consensus	*****	*****-*****	*****	*****	*****
msa185284.2{271_090}	AAAgcCTTGT	GCcTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_H36B}	AAAgcCTTGT	GCcTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_JM9130013}	AAAgcCTTGT	GCcTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_A909}	AAAgcCTTGT	GCcTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_CJB110}	AAAgcCTTGT	GCcTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_18RS21}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_2603}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M732}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M781}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_COH1}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_1169NT}	AAAtCTTGT	GCCcAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
Consensus	***-*****	***-*****	*****	*-*****	*****

Table 62: Comparative Sequences relating to SAG0690

	751	800
msa185284.2{271_090}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_H36B}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_JM9130013}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_A909}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_CJB110}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_18RS21}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_2603}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_M732}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_M781}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_COH1}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_1169NT}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
Consensus	*****	*****
	801	816
msa185284.2{271_090}	tCATTTGGAA AATAAA	
msa185284.2{271_H36B}	tCATTTGGAA AATAAA	
msa185284.2{271_JM9130013}	tCATTTGGAA AATAAA	
msa185284.2{271_A909}	tCATTTGGAA AATAAA	
msa185284.2{271_CJB110}	tCATTTGGAA AATAAA	
msa185284.2{271_18RS21}	tCATTTGGAA AATAAA	
msa185284.2{271_2603}	tCATTTGGAA AATAAA	
msa185284.2{271_M732}	nCATTTGGAA AATAAA	
msa185284.2{271_M781}	tCATTTGGAA AATAAA	
msa185284.2{271_COH1}	gCATTTGGAA AATAAA	
msa185284.2{271_1169NT}	tCATTTGGAA AATAAA	
Consensus	..*****	*****

SEQ ID NO. 6212

STRAIN 2603 frame: 1

MILKICRAAYSLQWGGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHL
AKIVHFLKYNSTFFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA
VKAFNKPAEVLVKDKRNAAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG
FKPGVSVFHFYQDI INHPDSI FDGYHPAKI KNQLSLAEHLVACVIPKHYQEDYQSLVPND
LKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6213

STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQDDKHLTKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSVFHFYQDI INHPDSI
FDGYHPAKI KNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6214

STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQDDKHLTKIVHFLKYNSTFFPYIPKYREAAATFN
EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDY
VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSVFHFYQDI INHPDSI FDGYHPA
KI KNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCH
LENK

SEQ ID NO. 6215

STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSVFHFYQDI INHPDSI
FDGYHPAKI KNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6216

STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSVFHFYQDI INHPDSI
FDGYHPAKI KNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLXHLLENK

SEQ ID NO. 6217

STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSVFHFYQDI INHPDSI
FDGYHPAKI KNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLWHLENK

SEQ ID NO. 6218

STRAIN M781 frame: 1

Table 62: Comparative Sequences relating to SAG0690

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDI INHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFYQDI INHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYREAAATF
 NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFD
 YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDI INHPDSIFDGYHP
 AKIKNQLSLAEHLVACVIPKHYQEDYQNLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLC
 HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYREAAATFNEDGISLT
 SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDYVMLNWSN
 TNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFYQDI INHPDSIFDGYHPAKIKNQLS
 LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYREA
 AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPK
 DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFYQDI INHPDSIFD
 GYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVY
 DFLCHLENK

PRETTY of: /biotmp/msa185358.2{*} May 13, 2003 07:11 ..

	1		50
msa185358.2{271_090}	-----	---dyplika felerIGAFI	AYEKQYKRKi
msa185358.2{271_JM9130013}	-----	-----IGAFI	AYEKQYKRKi
msa185358.2{271_H36B}	-----	-----ka felerIGAFI	AYEKQYKRKi
msa185358.2{271_A909}	-----	-LLdyprika felerIGAFI	AYEKQYKRKi
msa185358.2{271_CJB110}	-----	-LLdyprika felerIGAFI	AYEKQYKRKi
msa185358.2{271_1169NT}	-----	-----ika felerIGAFI	AYEKQYKRKt
msa185358.2{271_18RS21}	-----	-LLdyprika felerIGAFI	AYEKQYKRKt
msa185358.2{271_2603}	milkcraay slqwggyvql	aLLdyprika felerIGAFI	AYEKQYKRKt
msa185358.2{271_M732}	-----	-LLdyprika felerIGAFI	AYEKQYKRKt
msa185358.2{271_M781}	-----	-LLdyprika felerIGAFI	AYEKQYKRKt
msa185358.2{271_COH1}	-----	-LLdyprika felerIGAFI	AYEKQYKRKt
Consensus	*****	*****	*****
	51		100
msa185358.2{271_090}	EQCDDKHLL tKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_JM9130013}	EQCDDKHLL tKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_H36B}	EQCDDKHLL tKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_A909}	EQCDDKHLL tKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_CJB110}	EQCDDKHLL tKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_1169NT}	EQCDDKHLL aKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_18RS21}	EQCDDKHLL aKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_2603}	EQCDDKHLL aKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_M732}	EQCDDKHLL aKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_M781}	EQCDDKHLL aKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
msa185358.2{271_COH1}	EQCDDKHLL aKIVHFLKYN	SFTFPYIPKY REAAATFNED	GISLTSDFLS
Consensus	*****	*****	*****
	101		150
msa185358.2{271_090}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_JM9130013}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_H36B}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_A909}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_CJB110}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_1169NT}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_18RS21}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_2603}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_M732}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_M781}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM
msa185358.2{271_COH1}	HTCTIETAKL IFKEGKILSA	VKAFNKPAEV LVnDKRNAAG	DPKDYFDYVM

Table 62: Comparative Sequences relating to SAG0690

Consensus	*****	*****	*****	**-*****	*****
	151				200
msa185358.2{271_090}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_JM9130013}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_H36B}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_A909}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_CJB110}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_1169NT}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_18RS21}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_2603}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_M732}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_M781}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_COH1}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
Consensus	*****	*****	*****-	*****-	*****
	201				250
msa185358.2{271_090}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_JM9130013}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_H36B}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_A909}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_CJB110}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_1169NT}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQnLVPND	LKHRVYYLDY
msa185358.2{271_18RS21}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_2603}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M732}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M781}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_COH1}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
Consensus	*****	*****	*****	****-*****	*****
	251		272		
msa185358.2{271_090}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_JM9130013}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_H36B}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_A909}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_CJB110}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_1169NT}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_18RS21}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_2603}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_M732}	CNETLYEWNQ	KVYDFLxHLE	NK		
msa185358.2{271_M781}	CNETLYEWNQ	KVYDFLcHLE	NK		
msa185358.2{271_COH1}	CNETLYEWNQ	KVYDFLwHLE	NK		
Consensus	*****	*****-****	**		

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6301

STRAIN 2603

ATGAAAAGTCGAAAAAAGATAAATTGGTATTGAGGTAAACAACAACACTATTGGTTTTT
GGTTTTGGGTGGGGTTTTGGTTTTTATAATTATAAAAAATGATAATGTCGAACCGACAGTCACT
AGTGCATCGGATCAAACGACGACTTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATT
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAATCATCC
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAATATGACT
CAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT
GAGTTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAATCAAATACCTCTTCTTATAAG
GATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
AACCAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302

STRAIN 090

GGGGTTTTGGTTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303

STRAIN A909

GGGGTTTTGGTTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGCTTGGAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6304

STRAIN H36B

GGGGTTTTGGTTTTTATAATTATAAAAAATGATA
ATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT
CAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTA
TGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAATCATCCAGTGGACAAT
CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGG
CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCT
GCTTGGAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAAC
AGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTA
TTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6305

STRAIN 18RS21

GGGGTTTTGGTTTTTATAATTATAAAAAATGATAATG
TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
ACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGC
GTCAGTCTTATTAGCACAAAGCTATTTTGGAATCATCCAGTGGACAATCAG
ATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATAT
AAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAA
TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTT
TGGAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGG
TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTA
AAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6306

STRAIN M732

GGGGTTTTGGTTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6307

STRAIN COH1

GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTGGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6308

STRAIN M781

GGGGTTTGGTTTTATAATTATAAAAAATGA
TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA
TTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTG
TATGCGTCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACA
ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG
AATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAA
GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC
TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCAT
CTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTA
ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAAT
TATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309

STRAIN CJB110

GGGGTTTGGTTTTATAATTATAAAAAATGATAATGT
CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310

STRAIN 1169NT

GGGGTTTGGTTTTATAATTATAAAAAATGATAATGT
CGAACGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
CGATTTCCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311

STRAIN JM9130013

TTTGGTTTTATAATTATAAAAAATGATAATGTGGAACCGACAGTCACTAGT
GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCAACAGCTAT
TGAAATTTCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAG
CTATTTTGAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT
TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAAATCTGTTCAAAT
GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC
CTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAG
TTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTC
TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG
CTTATGCTAGTAAATTAAACCAAATTATTGAAACTACAGTCTAGATGCT
TATGATAAA

PRETTY of: /biotmp/msa243324.2{*} February 11, 2003 05:11 ..

	1				50
msa243324.2{275_A909}	-----	-----	-----	-----	-----
msa243324.2{275_H36B}	-----	-----	-----	-----	-----
msa243324.2{275_090}	-----	-----	-----	-----	-----
msa243324.2{275_18RS21}	-----	-----	-----	-----	-----
msa243324.2{275_2603}	atgaaaagtc	gaaaaaaaga	taaattggta	ttgaggttaa	caacaacact
msa243324.2{275_CJB110}	-----	-----	-----	-----	-----
msa243324.2{275_COH1}	-----	-----	-----	-----	-----
msa243324.2{275_M732}	-----	-----	-----	-----	-----

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M781}	-----	-----	-----	-----	-----
msa243324.2{275_1169NT}	-----	-----	-----	-----	-----
msa243324.2{275_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa243324.2{275_A909}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_H36B}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_090}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_18RS21}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_2603}	attgggttttt	gggtttgggtg	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_CJB110}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_COH1}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_M732}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_M781}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_1169NT}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_JM9130013}	-----	---TTTGGTT	TTATAATTAT	AAAAATGATA	
Consensus	*****	*****	*****	*****	*****
	101				150
msa243324.2{275_A909}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_H36B}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_090}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_18RS21}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_2603}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_CJB110}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_COH1}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M732}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M781}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_1169NT}	ATGTCGAACa	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_JM9130013}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
Consensus	*****	*****	*****	*****	*****
	151				200
msa243324.2{275_A909}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_H36B}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_090}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_18RS21}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_2603}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_CJB110}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_COH1}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M732}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M781}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_1169NT}	CAAACGATTT	CcCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_JM9130013}	CAAACGATTT	CcCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
Consensus	*****	*-*****	*****	*****	*****
	201				250
msa243324.2{275_A909}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_H36B}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_090}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_18RS21}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_2603}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_CJB110}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_COH1}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_M732}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_M781}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_1169NT}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_JM9130013}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
Consensus	*****	*****	*****	*****	*****
	251				300
msa243324.2{275_A909}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_H36B}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_090}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_18RS21}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_2603}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_CJB110}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_COH1}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_M732}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_M781}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_1169NT}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
msa243324.2{275_JM9130013}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCTTTGGCAT	CAAAGGAGAA
Consensus	*****	*****	*****	*****	*****
	301				350
msa243324.2{275_A909}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_H36B}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_090}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_18RS21}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_2603}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_CJB110}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_COH1}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M732}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_M781}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_1169NT}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_JM9130013}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
Consensus	*****	*****_**	*****	*****	*****
msa243324.2{275_A909}	351	CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_H36B}	400	CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_090}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_18RS21}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_2603}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_CJB110}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_COH1}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M732}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M781}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_1169NT}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_JM9130013}		CAAATCCAAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
Consensus	-*****-	*****	*****	*****	*****
msa243324.2{275_A909}	401	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_H36B}	450	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_090}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_18RS21}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_2603}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_CJB110}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_COH1}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_M732}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_M781}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_1169NT}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
msa243324.2{275_JM9130013}		CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA
Consensus	*****	*****	*****	*****	*****
msa243324.2{275_A909}	451	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_H36B}	500	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_090}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_18RS21}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_2603}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_CJB110}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_COH1}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_M732}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_M781}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_1169NT}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
msa243324.2{275_JM9130013}		GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG
Consensus	*-*****	*****_**	*****	*****	*****
msa243324.2{275_A909}	501	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_H36B}	550	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_090}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_18RS21}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_2603}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_CJB110}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_COH1}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_M732}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_M781}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_1169NT}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
msa243324.2{275_JM9130013}		AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA
Consensus	*****	*****	*****	*****	*****
msa243324.2{275_A909}	551	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_H36B}	582	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_090}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_18RS21}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_2603}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_CJB110}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_COH1}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_M732}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_M781}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_1169NT}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
msa243324.2{275_JM9130013}		TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA
Consensus	*****-***	*****	*****	*****	**

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRKKDKLVRLRLTTLLVFLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEI
 SKTYDLYASVLLAQAILSSSGQSDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMT
 QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKL
 NQIIETYSLDAYDK

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6313

STRAIN 090 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6314

STRAIN A909 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6315

STRAIN H36B frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6316

STRAIN 18RS21 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6317

STRAIN M732 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6318

STRAIN M781 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6319

STRAIN CJB110 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6320

STRAIN 1169NT frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
 SDLSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
 SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSldAYDK

SEQ ID NO. 6321

STRAIN JM9130013 frame: 3

WFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQSD
 LSKAPNYNLFGIKGEYKGKSVQMPtleDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS
 QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSldAYDK

PRETTY of: /biotmp/msa243476.2{*} February 11, 2003 05:17 ..

	1				50
msa243476.2{275_090}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_18RS21}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_2603}	mksrkkdklv	lrltttllvf	glggvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_CJB110}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_M732}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_M781}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_A909}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_H36B}	-----	-----	---gvWFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_JM9130013}	-----	-----	---WFYNY	KNDNVEpTVT	SASDQTTTTFI
msa243476.2{275_1169NT}	-----	-----	---gvWFYNY	KNDNVEqTVT	SASDQTTTTFI
Consensus	*****	*****	***_*****	*****_***	*****
	51				100
msa243476.2{275_090}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_18RS21}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_2603}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_CJB110}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_M732}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_M781}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_A909}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_H36B}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_JM9130013}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_1169NT}	QTISPTAIEI	SKTYDLYASV	LLAQAILESS	SGQSDLSKAP	NYNLFGIKGE
Consensus	*****	*****	*****	*****	*****

Table 63: Comparative Sequences relating to SAG1912

	101				150
msa243476.2{275_090}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_18RS21}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_2603}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_CJB110}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M732}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M781}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_A909}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_H36B}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_JM9130013}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_1169NT}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
Consensus	*****	*****	*****	*****	*****
	151				194
msa243476.2{275_090}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_18RS21}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_2603}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_CJB110}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M732}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M781}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_A909}	aWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_H36B}	aWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_JM9130013}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_1169NT}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
Consensus	-*****	*****	*****	*****	*****

Table 64: Comparative Sequences relating to SAG 0827

SEQ ID NO. 6401

STRAIN 2603

ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA
 TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
 ATGCTTCCAAATTCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTT
 GGCCCTTTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
 GAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT
 ATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAA
 CTTCTAGGAGTTCTAGATTTAGATTCTTCTTTAGTAGCAGATTATGATGAGATTGATCAA
 GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATG
 TTTGGAGTTGAAAAG

SEQ ID NO. 6402

STRAIN 090

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
 TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
 AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGCCCTTTCCAGG
 GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
 TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
 TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA
 TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCTTTA
 GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
 TATTCTAGTAGAACATACGATTGGAATTTGGATA

SEQ ID NO. 6403

STRAIN A909

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA
 CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTAT
 TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTTTTC
 CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG
 TGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
 ATGCTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTA
 CCTATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTC
 TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG
 TAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTT
 GAAAAG

SEQ ID NO. 6404

STRAIN H36B

CTCTATTCTCAGATGAAACAAATGCTCTTGCC
 CAACTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTG
 TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCT
 TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGT
 TGGTGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
 AGCATGCTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTA
 GTACCTATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCT
 TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT
 TTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAG
 GTTGAAAAG

SEQ ID NO. 6405

STRAIN 18RS21

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
 ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
 CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTTTTCAG
 GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
 ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
 CTAACCTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCT
 ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCTTT
 AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
 GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA
 AAG

SEQ ID NO. 6406

STRAIN M732

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
 ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
 CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGCCCTTTTCAG
 GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
 ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
 CTAACCTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCT
 ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCTTT
 AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
 GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA
 AAG

SEQ ID NO. 6407

STRAIN COH1

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACT
 TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATT
 TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGCCCTTTTC
 AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT

Table 64: Comparative Sequences relating to SAG 0827

GAATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA
TGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTAC
CCATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCT
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT
AGGTATTCTAGTAGAACATACGATTTGGAAATTTGGATATGTTTGGAGTTG
AAAAG

SEQ ID NO. 6408

STRAIN M781

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6409

STRAIN CJB110

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAAATTTGGATATGTTTGGAGTTGAA
AG

SEQ ID NO. 6410

STRAIN 1169NT

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCCA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAAATTTGGATATGTTTGGAGTTGAA
AG

SEQ ID NO. 6411

STRAIN JM9130013

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAAATTTGGATATGTTTGGAGTTGAA
AG

PRETTY of: /biotmp/msa236796.2{*} February 11, 2003 02:42 ..

	1				50
msa236796.2{282_COH1}	-----	-----	-----	-----	-----
msa236796.2{282_M732}	-----	-----	-----	-----	-----
msa236796.2{282_M781}	-----	-----	-----	-----	-----
msa236796.2{282_090}	-----	-----	-----	-----	-----
msa236796.2{282_CJB110}	-----	-----	-----	-----	-----
msa236796.2{282_18RS21}	-----	-----	-----	-----	-----
msa236796.2{282_2603}	atgaacaagt	ctaagaaaat	cgaaaattat	caattattat	tactacaage
msa236796.2{282_A909}	-----	-----	-----	-----	-----
msa236796.2{282_H36B}	-----	-----	-----	-----	-----
msa236796.2{282_JM9130013}	-----	-----	-----	-----	-----
msa236796.2{282_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa236796.2{282_COH1}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M732}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M781}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_090}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_CJB110}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_18RS21}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_2603}	gcaagCTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_A909}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_H36B}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_JM9130013}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_1169NT}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
Consensus	*****	*****	*****	*****	*****
msa236796.2{282_COH1}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_M732}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_M781}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_090}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_CJB110}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_18RS21}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_2603}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_A909}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_H36B}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_JM9130013}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
msa236796.2{282_1169NT}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT
Consensus	*****	*****	*****	*****	*****
msa236796.2{282_COH1}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_M732}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_M781}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_090}	TATTTATTTG	ATGGAAAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_CJB110}	TATTTATTTG	ATGGAAAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_18RS21}	TATTTATTTG	ATGGAgAaGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_2603}	TATTTATTTG	ATGGAgAaGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_A909}	TATTTATTTG	ATGGAgAaGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_H36B}	TATTTATTTG	ATGGAgAaGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_JM9130013}	TATTTATTTG	ATGGAgAaGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
msa236796.2{282_1169NT}	TATTTATTTG	ATGGAgAaGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT
Consensus	*****	*****-*-**	*****	*****-*	*****
msa236796.2{282_COH1}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_M732}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_M781}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_090}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_CJB110}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_18RS21}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_2603}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_A909}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_H36B}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_JM9130013}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
msa236796.2{282_1169NT}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC
Consensus	*****	*****	*****	*****	*****
msa236796.2{282_COH1}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_M732}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_M781}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_090}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_CJB110}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_18RS21}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_2603}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_A909}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_H36B}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_JM9130013}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
msa236796.2{282_1169NT}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT
Consensus	*****	*****-*	*****	*****	*****
msa236796.2{282_COH1}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_M732}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_M781}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_090}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_CJB110}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_18RS21}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_2603}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_A909}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_H36B}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_JM9130013}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
msa236796.2{282_1169NT}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA
Consensus	*****	*****	*****	*****	*-*****
msa236796.2{282_COH1}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_M732}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_M781}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_090}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_CJB110}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_18RS21}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_2603}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_A909}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_H36B}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_JM9130013}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_1169NT}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
Consensus	*****	*****	*****	*****	*****
401					
msa236796.2{282_COH1}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_M732}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_M781}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_090}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_CJB110}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_18RS21}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_2603}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_A909}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_H36B}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_JM9130013}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
msa236796.2{282_1169NT}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTTGT	AGGTATTCTA
Consensus	*****	*****	*****	*****	*****
451					
msa236796.2{282_COH1}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTTGGAA	TTTGGATA--	-----	-----
msa236796.2{282_CJB110}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTTGGAA	TTTGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	-----	-----

SEQ ID NO. 6412

STRAIN 2603 frame: 1

MNKSCKIENYQLLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELIL
 GPFQGGVSCVHITLKGKVCGESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGK
 LLGVLDLDDLSSLVADYDEIDQEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6413

STRAIN 090 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID
 QEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6414

STRAIN A909 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID
 QEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6415

STRAIN H36B frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID
 QEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6416

STRAIN 18RS21 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID
 QEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6417

STRAIN M732 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID
 QEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6418

STRAIN COH1 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID
 QEYLEKFVGIWNLDMFGVEK

SEQ ID NO. 6419

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFEDGEELILGPFQGGVSCVHITLKGKVC
 GESAQTAKTILVDDVTKHANYISCDISKAMSEIVVPMFKNGKLLGVLDLDDLSSLVADYDEID

Table 64: Comparative Sequences relating to SAG 0827

QEYLEKFVGILVEHTIWNLD MFGVEK

SEQ ID NO. 6420

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLF DGEELILGPFQGGVSCVHITLGKGV C
 GESAQTAKTLIVDDVTKHANYISCD SKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
 QEYLEKFVGILVEHTIWNLD MFGVEK

SEQ ID NO. 6421

STRAIN CJB110 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLF DGEELILGPFQGGVSCVHITLGKGV C
 GESAQTAKTLIVDDVTKHANYISCD SKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
 QEYLEKFVGILVEHTIWNLD MFGVEK

SEQ ID NO. 6422

STRAIN 1169NT frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLF DGEELILGPFQGGVSCVHITLGKGV C
 GESAQTAKTLIVDDVTKHANYISCD SKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
 QEYLEKFVGILVEHTIWNLD MFGVEK

SEQ ID NO. 6423

STRAIN JM9130013 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLF DGEELILGPFQGGVSCVHITLGKGV C
 GESAQTAKTLIVDDVTKHANYISCD SKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
 QEYLEKFVGILVEHTIWNLD MFGVEK

PRETTY of: /biotmp/msa237960.2{*} February 11, 2003 02:46 ..

	1				50
msa237960.2{282_1169NT}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_18RS21}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_2603}	mnkskkieny qllllqaqaL	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_A909}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_COH1}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_H36B}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_JM9130013}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_M732}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_M781}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_090}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
msa237960.2{282_CJB110}	-----L	FSDETNALAN	LSNASAMLNA	MLPNSVFTGF	
Consensus	*****	*****	*****	*****	*****
	51				100
msa237960.2{282_1169NT}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_18RS21}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_2603}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_A909}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_COH1}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_H36B}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_JM9130013}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_M732}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_M781}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_090}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
msa237960.2{282_CJB110}	YLF DGeELIL	GPFQGGVSCV	HITLGKGVCG	ESAQTAKTLI	VDDVTKHANY
Consensus	*****	*****	*****	*****	*****
	101				150
msa237960.2{282_1169NT}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_18RS21}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_2603}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_A909}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_COH1}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_H36B}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_JM9130013}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_M732}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_M781}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_090}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
msa237960.2{282_CJB110}	ISCDSKAMSE	IVVPMFKNGK	LLGVLDLDSS	LVADYDEIDQ	EYLEKFVGIL
Consensus	*****	*****	*****	*****	*****
	151				165
msa237960.2{282_1169NT}	VEHTIWNLDm	fgvek			
msa237960.2{282_18RS21}	VEHTIWNLDm	fgvek			
msa237960.2{282_2603}	VEHTIWNLDm	fgvek			
msa237960.2{282_A909}	VEHTIWNLDm	fgvek			
msa237960.2{282_COH1}	VEHTIWNLDm	fgvek			
msa237960.2{282_H36B}	VEHTIWNLDm	fgvek			
msa237960.2{282_JM9130013}	VEHTIWNLDm	fgvek			
msa237960.2{282_M732}	VEHTIWNLDm	fgvek			
msa237960.2{282_M781}	VEHTIWNLDm	fgvek			
msa237960.2{282_090}	VEHTIWNLD-	~~~~~			
msa237960.2{282_CJB110}	VEHTIWNLDm	fgvek			
Consensus	*****	-----			

Table 65: Comparative Sequences relating to SAG0231**SEQ ID NO. 6501****STRAIN 2603**

ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA
 TTATTTCATACTTGTTTTTAGCGGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
 CTAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG
 AATATAGAAGAAATAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT
 TGTACTGTAAAGATTTTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT
 TTGGAATCGAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
 TCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTTCAGATGGTCAGGAGAAG
 ATACAA

SEQ ID NO. 6502**STRAIN 090**

GGAGGATTTTATATGAAAGAACA
 ACAAGAAAAGAAGAACTAAAACCGGAATCGAGAATATGAAGTTAGTCTAG
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
 AATCGAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTT
 TTTGATTCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTC
 AGATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6503**STRAIN A909**

GGAGGATTTTATATGAAAGAACAACA
 AGAAAAGAAGAACTAAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAA
 AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCA
 TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC
 GAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTTTG
 ATTCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTCAGAT
 GGTCAGGAGAAGATaCAA

SEQ ID NO. 6504**STRAIN H36B**

GGAGGATTTTATATGAAAGAACA
 ACAAGAAAAGAAGAACTAAAACCGGAATCGAGAATATGAAGTTAGTCTAG
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
 AATCGAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTT
 TTTGATTCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTC
 AGATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6505**STRAIN 18RS21**

GGAGGATTTTATATGAAAGAACAAC
 AAAGAAAAGAAGAACTAAAACCGGAATCGAGAATATGAAGTTAGTCTAGTC
 AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACA
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATT
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
 TCGAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTT
 TGATTCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTCAG
 ATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6506**STRAIN M781**

GGAGGATTTTATATGAAAGAACAACAAAGAAAA
 GAAGAACTAAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT
 GAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTT
 CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATTTAAT
 GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA
 AAATTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAA
 GAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAG
 GAGAAGATACAA

SEQ ID NO. 6507**STRAIN CJB110**

GGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
 CTAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA
 TTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTTCAACTG
 AAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATTTAATGATAAA
 AAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAATTA
 TAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAGAATTG
 GTAAAACAAAAAACTATAAAAAATTATTTTTTTCAGATGGTCAGGAGAAG
 ATACAA

SEQ ID NO. 6508**STRAIN 1169NT**

GGAGGATTTTATATGAAAGAACAACAAG
 AAAAGAAGAACTAAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG
 CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCT

Table 65: Comparative Sequences relating to SAG0231

GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATT
 TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA
 AAAAAATTATAGTGGAAAATTTAATGAAAAAATATGAATTTTTTTGAT
 TCAAGAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGG
 TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTTATATGAAAGAACAAC

AAAGAAAAGAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTC

AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACA

TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT

CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA

TCGAAAAAAATTTATAGCGGAAAATTTAATGAAAAAATATGAATTTTTT

TGATTCAAGAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAG

AtGGtCAGGAGAAGATACAA

PRETTY of: /biotmp/msa75400.2{*} March 10, 2003 09:56 ..

	1				50
msa75400.2{286_090}	-----	-----	-----	-----	-----
msa75400.2{286_CJB110}	-----	-----	-----	-----	-----
msa75400.2{286_18RS21}	-----	-----	-----	-----	-----
msa75400.2{286_2603}	atgaaaaaga	gtaccccaat	aataactacta	atagttgcat	tattcatact
msa75400.2{286_A909}	-----	-----	-----	-----	-----
msa75400.2{286_H36B}	-----	-----	-----	-----	-----
msa75400.2{286_JM9130013}	-----	-----	-----	-----	-----
msa75400.2{286_M781}	-----	-----	-----	-----	-----
msa75400.2{286_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa75400.2{286_090}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_CJB110}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_18RS21}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_2603}	tggttttagc	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_A909}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_H36B}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_JM9130013}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_M781}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_1169NT}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa75400.2{286_090}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_CJB110}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_18RS21}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_2603}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_A909}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_H36B}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_JM9130013}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_M781}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_1169NT}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa75400.2{286_090}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_CJB110}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_18RS21}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_2603}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_A909}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_H36B}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_JM9130013}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_M781}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_1169NT}	TCCTATGAGA	ATATAGAAGA	AATAAAAATC	ACACATCCTG	TTTCAACTGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa75400.2{286_090}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_CJB110}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_18RS21}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_2603}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_A909}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_H36B}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_JM9130013}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_M781}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_1169NT}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa75400.2{286_090}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_CJB110}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_18RS21}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT

Table 65: Comparative Sequences relating to SAG0231

msa75400.2{286_2603}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_A909}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_H36B}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_JM9130013}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_M781}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_1169NT}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
Consensus	*****	*****	*****	*****	*****
msa75400.2{286_090}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_CJB110}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_18RS21}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_2603}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_A909}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_H36B}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_JM9130013}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_M781}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_1169NT}	AGcGGAAAtT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
Consensus	**_*****	*****	*****	*****	*****
msa75400.2{286_090}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_CJB110}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_18RS21}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_2603}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_A909}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_H36B}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_JM9130013}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_M781}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_1169NT}	TAAAACAAAA	AAAACATAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
Consensus	*****	*****	*****	*****	*****
msa75400.2{286_090}	TACAA				
msa75400.2{286_CJB110}	TACAA				
msa75400.2{286_18RS21}	TACAA				
msa75400.2{286_2603}	TACAA				
msa75400.2{286_A909}	TACAA				
msa75400.2{286_H36B}	TACAA				
msa75400.2{286_JM9130013}	TACAA				
msa75400.2{286_M781}	TACAA				
msa75400.2{286_1169NT}	TACAA				
Consensus	*****				
SEQ ID NO. 6510					
STRAIN 2603 frame: 1					
MKKSTQIILLIVALFILVSGGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKI					
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTK					
KTIKIIIFSDGQEKIQ					
SEQ ID NO. 6511					
STRAIN 090					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD					
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ					
EKIQ					
SEQ ID NO. 6512					
STRAIN A909					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH					
CTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK					
IQ					
SEQ ID NO. 6513					
STRAIN H36B					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD					
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ					
EKIQ					
SEQ ID NO. 6514					
STRAIN 18RS21					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW					
HCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ					
KIQ					
SEQ ID NO. 6515					
STRAIN CJB110					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK					
ISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEKIQ					
SEQ ID NO. 6516					
STRAIN JM9130013					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW					

Table 65: Comparative Sequences relating to SAG0231

HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIIFSDGQE
KIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIIFSDGQEKIQ

PRETTY of: /biotmp/msa75376.2{*} March 10, 2003 10:01 ..

	1				50
msa75376.2{286_090}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_1169NT}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_18RS21}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_2603}	mkkstqiill	ivalfilvfs	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_A909}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_CJB110}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_H36B}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_JM9130013}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_M781}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
Consensus	*****	*****	*****	*****	*****

	51				100
msa75376.2{286_090}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_1169NT}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_18RS21}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_2603}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_A909}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_CJB110}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_H36B}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_JM9130013}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_M781}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
Consensus	*****	*****	*****	*****	*****

	101				135
msa75376.2{286_090}	SGnFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_1169NT}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_18RS21}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_2603}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_A909}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_CJB110}	SGnFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_H36B}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_JM9130013}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
msa75376.2{286_M781}	SGkFNEKNMN	FFDSRIGTK	KTIKIIFSDG	QEKIQ	
Consensus	**_*****	*****	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6601

STRAIN 2603

TTGACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATG
GAAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAGCAGCGCTT
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAG
GATCCTAGATTAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGAT
GAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTCAAAAAATCAAATACCA
AAGTTAGTTTATATTTTCAGCCAACAGCGGCTATTTCAGCTTACATTAAAAGTAAAAGGAAG
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATG
TATGGTGAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGATAGTGGCA
GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAA
TTAAATAATAAA

SEQ ID NO. 6602

STRAIN 090

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC
AAGTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTA
TTTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAA
ATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6603

STRAIN A909

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC
AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
ACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTAT
TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAA
TCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6604

STRAIN H36B

TATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATGG
AAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA
GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
TAAAGGTGATATATTTAAGGATCCTAGATTAACTTACATTAGGGGAGATA
TTACAGAAGCTGATAAGATTCAATTTAGAAGACAGAACTTTTGATATATTA
ATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGATGAGCTTAACGT
TAAAGCAACCCAAAAAGCAGTAGCACTCTGTCAAAAAATCAAATACCAA
AGTTAGTTTATATTTTCAGCCAACAGCGGCTATTTCAGCTTACATTAAAAGT
AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT
TGTAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTTCC
AAGCCAAGTGTATAAAGTTATTTAGTCATTTGCCCTTTCTTAGGTATTGTT
GTACAAAAGGTCTTTCCAACCTAAGGTTGTGATAGTGGCAGAAGCAATCGT
TACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAAT
TAAATAATAAA

SEQ ID NO. 6605

STRAIN 18RS21

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTA
TTTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAA
ATCCTTTCTATTGAAGAATTAAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6606

STRAIN M732

CAAAATGAAGGAGAGGGAAGTATGgAAATACTGATTGCAGGTGGTAGTGG
TTTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGG
TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCT
AGATTAACTTACATTAAAGGGAGATATTACAGAAGCTGATAAGATTCAATTT
AGaACATAGAAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGC
CCAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCA
CTCTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTTCAGCCAATAG
CGGCTATTTCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCA
AAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGT
GAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAG
TCATTTGCCCTTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGG
TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACT
CAAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAAATTTCTATACTAAATTTAC
AAAATGAAGGAGAGGGAAGTATGGAAATACTGATTGCAGGTGGTAGTGGT
TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGT
GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA
GATTAACTTACATTAAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTA
GAACATAGAAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCC
CAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCAC
TCTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTTCAGCCAATAGC
GGCTATTTCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA
AGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTG
AAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGT
CATTTGCCCTTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGT
TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTC
AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAAATTTCTATACTAAATTTaCA
AAATGAAGGAGAGGGAAGTATGGAAATACTGATTGCAGGTGGTAGTGGTT
TTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTG
GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTAG
ATTAACCTTACATTAAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTAG
AACATAGAAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCC
AATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACT
CTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTTCAGCCAATAGCG
GCTATTTCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAA
GCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGA
AGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGTC
ATTTGCCCTTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGT
GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTCA
AAAAATCCTTTCTATGAAGAATTAAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAAGTATGGAAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTCACAAAAATCAAATACCAAAGTTAGTTTACATTTTCAGCCAACAGCGGC
TATTTCAGCTTACATTAGAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGTCAT
TTGCCCTTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAAGTATGGAAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGC
TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTCACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGC
TATTTCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAAGTTATTTAGTCAT
TTGCCCTTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6611

STRAIN JM9130013

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATG

AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA

GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA

CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA

CctACATTAGGGGAGATATTACAGAAGCTGATAAGATTTCATTTAGAAGAC

AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCA

ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTC

ACAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTAT

TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG

CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGTATGGTGAAGAGC

GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAATTTG

CCTTTCTTAGGTATTGTTGTACAAAAGGCTTTTCCAATAAGGTTGTGAT

AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACCCAAAAA

TCCTTTCTATTGAAGAATTAAATAATAA

PRETTY of: /biotmp/msa137119.2{*} April 10, 2003 03:30 ..

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1                                     50
msa137119.2{303_COH1} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_M732} -----CAAA ATGAAGGAGA
msa137119.2{303_m781} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_090} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_18RS21} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_2603} ttgacaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_A909} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_CJB110} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_H36B} -----tataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_JM9130013} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_1169NT} ---acaaggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
Consensus *****

51                                     100
msa137119.2{303_COH1} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
msa137119.2{303_M732} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
msa137119.2{303_m781} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
msa137119.2{303_090} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_18RS21} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_2603} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_A909} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_CJB110} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_H36B} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_JM9130013} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
msa137119.2{303_1169NT} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGgAAGC
Consensus *****

101                                    150
msa137119.2{303_COH1} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_M732} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_m781} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_090} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_18RS21} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_2603} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_A909} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_CJB110} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_H36B} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_JM9130013} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
msa137119.2{303_1169NT} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAGgTGGC TTACTTATCA
Consensus *****

151                                    200
msa137119.2{303_COH1} AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_M732} AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_m781} AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_090} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_18RS21} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_2603} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_A909} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_CJB110} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_H36B} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_JM9130013} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_1169NT} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
Consensus ***-*****

201                                    250
msa137119.2{303_COH1} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
msa137119.2{303_M732} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
msa137119.2{303_m781} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
msa137119.2{303_090} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
msa137119.2{303_18RS21} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
msa137119.2{303_2603} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT

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Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_A909}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_CJB110}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_H36B}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_JM9130013}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_1169NT}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
Consensus	***-*****	*****	*****	*****	-*-*****-*
msa137119.2{303_COH1}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_M732}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_m781}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_090}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_18RS21}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_2603}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_A909}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_CJB110}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_H36B}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_JM9130013}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_1169NT}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_M732}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_m781}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_090}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_18RS21}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_2603}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_A909}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_CJB110}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_H36B}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_JM9130013}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_1169NT}	GAGCTTAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_M732}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_m781}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_090}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_18RS21}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_2603}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_A909}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_CJB110}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_H36B}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_JM9130013}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_1169NT}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
Consensus	*****	*****	*-*****	***-*****	*****
msa137119.2{303_COH1}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_M732}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_m781}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_090}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_18RS21}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_2603}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_A909}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_CJB110}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_H36B}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_JM9130013}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_1169NT}	ACATTaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
Consensus	*****-***	*****	*****	*****	*****
msa137119.2{303_COH1}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_M732}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_m781}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_090}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_18RS21}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_2603}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_A909}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_CJB110}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_H36B}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_JM9130013}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_1169NT}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	CTCGATTTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_M732}	CTCGATTTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_m781}	CTCGATTTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_090}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_18RS21}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_2603}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_A909}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_CJB110}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_H36B}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_JM9130013}	CTCGATTTTC	CAAGCCAAGT	GTATAAAgTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_1169NT}	CTCGATTTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
Consensus	*****	*****	*****-*	*****	*****
551					
msa137119.2{303_COH1}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_M732}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_m781}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_090}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_18RS21}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_2603}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_A909}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_CJB110}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_H36B}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_JM9130013}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_1169NT}	TAGGTATTGT	TGTACAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
Consensus	*****	*****	*****	*****	*****
601					
msa137119.2{303_COH1}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAACtCAA	AAATCCTTTC
msa137119.2{303_M732}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAACtCAA	AAATCCTTTC
msa137119.2{303_m781}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAACtCAA	AAATCCTTTC
msa137119.2{303_090}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_18RS21}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_2603}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_A909}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_CJB110}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_H36B}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_JM9130013}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAA	AAATCCTTTC
msa137119.2{303_1169NT}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACtCAA	AAATCCTTTC
Consensus	*****	*****-****	*****-****	*****-****	*****
651					
msa137119.2{303_COH1}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_M732}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_m781}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_090}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_18RS21}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_2603}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_A909}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_CJB110}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_H36B}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_JM9130013}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_1169NT}	TATTGAAGAA	TTAAATAATA	AA		
Consensus	*****	*****	**		

SEQ ID NO. 6612

STRAIN 2603 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6613

STRAIN 090 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6614

STRAIN A909 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6615

STRAIN H36B frame: 2

IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKDPRL
 TYIRGDITEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPKLVY
 ISANSYGYSAYIKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFL
 GIVVQKVFP TKVVIVAEIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6616

Table 66: Comparative Sequences relating to SAG 0754

STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEAI VTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617

STRAIN M732 frame: 1

QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKDPRLTYIKGDI T
 EADKIHLEHRNFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPKLVYISANSYGYS
 AYIKSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL PFLGIVVQKV
 PTKVVIVAEAI VTSRLRKKPTQKILSIEELNNK

SEQ ID NO. 6618

STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIKGDI TEADKIHLEHRNFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEAI VTSRLRKKPTQKILSIEELNNK

SEQ ID NO. 6619

STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIKGDI TEADKIHLEHRNFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEAI VTSRLRKKPTQKILSIEELNNK

SEQ ID NO. 6620

STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDI FKD
 PRLTYIKGDI TEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIRSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEAI VTTLRKPTQKILSIEELNNK

SEQ ID NO. 6621

STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEAI VTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6622

STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEI IKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFP TKVVIVAEAI VTTLRKKPTQKILSIEELNNK

PRETTY of: /biotmp/msa137299.2{*} April 10, 2003 03:37 ..

	1		50
msa137299.2{303_COH1}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_M732}	----- -QNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_M781}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_090}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_18RS21}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_2603}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_A909}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_CJB110}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_JM9130013}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_H36B}	---ikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKvAYLSR
msa137299.2{303_1169NT}	trhikisiln lQNEGEGTME	ILIAGGSGFL GKQIIKAALT	KGHKLAYLSR
Consensus	----- *****	*****	*****
	51		100
msa137299.2{303_COH1}	HEGKGDI FKD PRLTYIKGDI	TEADKIHLEh RnFDILIDCI	GAIKPNQLDE
msa137299.2{303_M732}	HEGKGDI FKD PRLTYIKGDI	TEADKIHLEh RnFDILIDCI	GAIKPNQLDE
msa137299.2{303_M781}	HEGKGDI FKD PRLTYIKGDI	TEADKIHLEh RnFDILIDCI	GAIKPNQLDE
msa137299.2{303_090}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_18RS21}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_2603}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_A909}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_CJB110}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_JM9130013}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_H36B}	HEGKGDI FKD PRLTYIrGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_1169NT}	HEGKGDI FKD PRLTYIKGDI	TEADKIHLEd RtFDILIDCI	GAIKPNQLDE
Consensus	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

	101			150	
msa137299.2{303_COH1}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_M732}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_M781}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_090}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_18RS21}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_2603}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_A909}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_CJB110}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_JM9130013}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_H36B}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_1169NT}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIrSKRKA	EQI IKASGLD
Consensus	*****	*****	*****	****_****	*****
	151			200	
msa137299.2{303_COH1}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_M732}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_M781}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_090}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_18RS21}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_2603}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_A909}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_CJB110}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_JM9130013}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_H36B}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_1169NT}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
Consensus	*****	*****	*****	*****	*****
	201		223		
msa137299.2{303_COH1}	AIVT _s LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_M732}	AIVT _s LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_M781}	AIVT _s LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_090}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_18RS21}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_2603}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_A909}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_CJB110}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_JM9130013}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_H36B}	AIVT _t LRkKP	TQKILSIEEL	NNK		
msa137299.2{303_1169NT}	AIVT _t LrtKP	TQKILSIEEL	NNK		
Consensus	****_***_**	*****	***		

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6701

STRAIN 090

CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
GATGAGGATTTTTGTTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTGAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTG
AAGTTGTTTCAGGCTGCGGATGATAAAGATATTCTAGTTATGGAATTATCA
AGTTTTTCAGCTAATGGGAGTTAAGGAATTTCTGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATT
ATGTTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTT
TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTAC
TAAAGCAACAATCGTTCCCTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTTAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAACATATGTTGTTTGTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTTGAAGT
CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702

STRAIN A909

CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCTGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
GATGAGGATTTTTGTTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTGAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTG
AAGTTGTTTCAGGCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCA
AGTTTTTCAGCTAATGGGAGTTAAGGAATTTCTGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATT
ATGTTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTT
TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTAC
TAAAGCAACAATCGTTCCCTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAAAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAA
CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAACATATGTTGTTTGTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTTGAAGT
CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAACAATAACAACATTTGAAAAT
AAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG
TTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT
TTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAGTG
GTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTACAT
GATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGCAT
TAGAAAAACAAATCCCTGTTTTGACTGAAGTGAATTAGCATACTTAGTT
TCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAAC
GACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGTTTGT
TAGCTGGGAATATCGGCTTTCTGCTAGTGAAGTTGTTTCAGGCTGCGAAT
GATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGAGT
TAAGGAATTTCTGTCCTCATATTGCAGTAATTACTAATTTAATGCCAACTC
ATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGAAT
ATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTAATCA
AGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTTCCCTT
TCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAACTT
TTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATGGTGTCCCAGG
AAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGG
CTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGGAGGT
GTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTATTAGTTTCTA
TAACGACAGCAAG

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6704

STRAIN 18RS21

GGACGAGTAATGAAAAACAATAACAACATTTG
 AAAATAAAAAAGTTTTAGTCCCTTGGTTTAGCACGATCTGGAGAAGCTGCT
 GCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
 ACCATTTGATGAAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTA
 AAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT
 TACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
 AGCATTAGAAAAACAATCCCTGTTTGTACTGAAGTGGAATTAGCATACT
 TAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACG
 ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGG
 TTTGTTAGCTGGGAATATCGGCTTTCCCTGCTAGTGAAGTTGTTGAGGCTG
 CGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTGAGCTAATG
 GGAGTTAAGGAATTTCTCCTCATATTGCAGTAATTACTAATTTAATGCC
 AACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAAT
 GGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTT
 AATCAAGGTATTTCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGT
 TCCCTTCTCTACTACGGAATAAGTTGATGGTGCTTACGTACAAGACAAGC
 AACTTTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTGGTGTG
 CCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA
 ACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTG
 GAGGTGTTAAACACCGCTTGCATCACTCGGTAAGGTTGATGGTATTAGT
 TTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTT
 ATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATC
 GCGGTAATGAGTTTGTGATGAATTGATACCAGATATCACTGGACTTAAACAT
 ATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAA
 AGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATA
 AAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTTGCA
 AATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATT
 CATTGATACTTTGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705

STRAIN M732

GGACGAGTAATGAAAAACAATAACAACATTTGAAA
 ATAAAAAAGTTTTAGTCCCTTGGTTTAGCACGATCTGGAGAAGCCGCTGCA
 CGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACC
 ATTTGATGAAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAG
 TGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTAC
 ATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGC
 ATTAGAAAAACAATCCCTGTTTGTACTGAAGTGGAATTAGCATACTTAG
 TTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACA
 ACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGTTT
 GTTAGCTGGGAATATCGGCTTTCCCTGCTAGTGAAGTTGTTGAGGCTGCGG
 aTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTGAGCTAATGGGA
 GTTAAGGAATTTCTGCTCATATTGCAGTAATTACTAATTTAATGCCAAC
 TCAATTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGA
 ATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTAAT
 CAAGGTATTTCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGTTCC
 TTTCTCTACTACGGAATAAGTTGATGGTGCTTACGTACAAGACAAGCAAC
 TTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTGGTGTCCCA
 GGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACT
 AGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGGAG
 GTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTGATGGTATTAGTTTC
 TATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTATC
 TGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCGCG
 GTAATGAGTTTGTGATGAATTGATACCAGATATCACTGGACTTAAACATATG
 GTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAAGC
 AGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAG
 CTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTTGCAAAAT
 GCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATTCAT
 TGATACTTTGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706

STRAIN COH1

GGACGAGTAATGAAAAACAATAACAACATTTGA
 AAATAAAAAAGTTTTAGTCCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG
 CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
 CCATTTGATGAAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA
 AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTT
 ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
 GCATTAGAAAAACAATCCCTGTTTGTACTGAAGTGGAATTAGCATACTT
 AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGA
 CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGT
 TTGTTAGCTGGGAATATCGGCTTTCCCTGCTAGTGAAGTTGTTGAGGCTGC
 GGaTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTGAGCTAATGG
 GAGTTAAGGAATTTCTGCTCATATTGCAGTAATTACTAATTTAATGCCA
 ACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATG
 GAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTA
 ATCAAGGTATTTCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGTT
 CCTTTCTCTACTACGGAATAAGTTGATGGTGCTTACGTACAAGACAAGCA
 ACTTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTGGTGTCC
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

Table 67: Comparative Sequences relating to SAG0475

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG
 AGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTATTAGTT
 TCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATT
 TCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCG
 CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA
 TGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA
 GCAGGAGTAACCTTAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
 AGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAA
 ATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATTC
 ATTGATACTTTTCGAAA

SEQ ID NO. 6707

STRAIN M781

GGACGAGTAATGAAAACAATAACAACATT
 TGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCG
 CTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGC
 AAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTAT
 TAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTT
 GTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAA
 AAAGCATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATA
 CTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAA
 CGACAACGACAACGATGATTGCAGAAAGTCTTAAATGCTGGAGGTGAGAGA
 GGTGTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGC
 TGCGGATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTTCAGCTAA
 TGGGAGTTAAGGAATTTGTCCTCATATTGCAGTAATTACTAATTTAATG
 CCAACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAA
 ATGGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATT
 TTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAaCAATC
 GTTCTTTTCTACTACGGAAAAAGTTGATGGTGCCTTACGTACAAGACAA
 GCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTG
 TCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCT
 AAAGTCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTT
 TGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTATTA
 GTTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCA
 TTCTGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGA
 TCGCGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAAC
 ATATGGTTGTTTTAgGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAA
 AAAGCAGGAGTaACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACA
 TAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTG
 CAAATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAA
 TTCATTGATACTTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6708

STRAIN CJB110

GGACGAGTAATGAAAACAATAACAACATTTGA
 AAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG
 CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA
 CCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA
 AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTT
 ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAA
 GCATTAGAAAAACAATCCCTGTTTTGACTGAAGTGGAAATTAGCATACTT
 AGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA
 CAACGACAACGATGATTGCAGAAAGTCTTAAATGCTGGAGGTGAGAGAGGT
 TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGC
 GGATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTTCAGCTAATGG
 GAGTTAAGGAATTTGTCCTCATATTGCAGTAATTACTAATTTAATGCCA
 ACTCATTTAGATTATCATGGGTCTTTTGAAGAATATGTTGCTGCAAAATG
 GAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTA
 ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTT
 CCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA
 ACTTTTCTATAAAGGGGAGAATATTATGTTAGTAGATGACATTGGTGTCC
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA
 CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG
 AGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTATTAGTT
 TCTATAATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATT
 TCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCG
 CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA
 TGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA
 GCAGGAGTAACCTTAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
 AGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAA
 ATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATTC
 ATTGATACTTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
 TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAAAACATTTGATGAAAATCCAACAGCACAGTCTTTGT
 TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
 GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
 TCCTATGGTCAAAAAGCATTAGAAAAACAATCCCTGTTTTGACTGAAG
 TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
 TCTAACGGGAAAAACGACAACGACAACGATGATTGCAGAAAGTCTTGAATGC

Table 67: Comparative Sequences relating to SAG0475

TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG
 AAGTTGTTCAAGGCTGCCGATGATAAAGATACTCTAGTTATGGAATTATCA
 AGTTTTCAGCTAATGGGAGTTAAGGAATTTTCGTCCTCATATTGCAGTAAT
 TACTAATTTAATGCCAACTCATTAGATTATCATGGGTCTTTTGAAGAT
 ATGtTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT
 TTGGTACTTAATTTTAACTAAGGTATTTCTAAAGAGTTAGcTAAAACTAC
 TAAAGCAACAATCGTTCCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
 ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTA
 GACGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
 TATTGCCGTTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTTAAGCAATTTTGGAGGTGTAAACACCGCTTGCAATCACTCGGTAAG
 GTTCATGGTATTAGTTTCTATAACGACAGTAAGTCAACTAATATATTGGC
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
 CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
 ACTGGACTTAAGCATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
 ACGTGCTGCACAAAAGCAGGAGTAACCTATAGCAATGCTTTAGATGTTA
 GAgATGCgGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
 TTGTTmAGTcCTGCGAATGCATCATGGGACATGTATAAGAATTTCGAAGT
 CCGTGGTGATGAATTCTTGATACTTTTCG

SEQ ID NO. 6710

STRAIN JM9130013

GGACGAGTAATGAAAACAATAACAACA

TTTGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCACGATCTGGAGAAGC
 TGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATG
 GCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGT
 ATTAAGTGGTTTGTGGTAGTCATCTTTAGAATTGtTAGATGAGGATTT
 TTGTTACATGATTaAAAATCCAGGAATACCTTATAACAATCCTATGGTCA
 AAAAAGCATTAGAAAAACAATCCCTGTTTGAAGTGAAGTGAATTAGCA
 TACTTAGTTTcAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAA
 AACGACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGA
 GAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTGAAGTTGTTcAG
 GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTcAGCT
 AATGGGAGTTAAGGAATTTTCGTCCTCATATTGCAGTAATTACTAATTTAA
 TGCCAACCTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCA
 AAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAA
 TTTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCaCAA
 TCGTTCCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGAC
 AAGCAACTTTTCTATAAAGGGGAGAATATTATGTcAGTAGATGACATTGG
 TGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCCGTTG
 CTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAAT
 TTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTcATGGTAT
 TAGtTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAG
 CATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTT
 GATCGCAGTAATGAGTTTgATGAATTGATACCAGATATCACTGGACTTAA
 ACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCAC
 AAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTA
 CATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCC
 TGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATG
 AATTcATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6710

STRAIN 2603

ggacgagtaatgaaaacaataacaacatttgaaaataaaaaagtttttagt
 ccttggttttagcacgatctggagaagctgctgcacgtttggttagctaagt
 taggagcaatagtgcaggttaatgatggcaaacatttgatgaaaatcca
 acagcacagtccttggttggaagaggggtattaaagtgggtttggtggtagtca
 tccttttagaattggttagatgaggatttttggttacatgattaaaaatccag
 gaataccttataacaatcctatgggtcaaaaaagcattagaaaaacaatc
 cctggttttgactgaagtggatttagcatacttagtttcagaatctcagct
 aataggtattacaggtctaacgggaaaacgacaacgacaacgatgattg
 cagaagtcttaaatgctggaggtcagagaggtttggttagctgggaatatc
 ggctttcctgctagtgaagttggttcaggctgcgaatgataaagatactct
 agttatggaattatcaagttttcagctaatgggagtttaagggaatttcgtc
 ctcatattgcagtaattactaatttaatgccaaactcatttagattatcat
 ggggtcttttgaagattatggtgctgcaaaatggaatatccaaaatcaa
 gtcttcatctgattttttgggtacttaatttttaatacaagggtatttctaaag
 agttagctaaaaactactaaagcaacaatcgttccctttctctactacggaa
 aaagttgatgggtgcttacgtacaagacaagcaactttctataaaggggga
 gaataattatgtcagtagatgacattgggtgtcccagggaagccataacgtag
 agaatgctctagcaactattgcgggtgctaaactggctgggtatcagta
 caagttatttagagaaactttaagcaattttggaggtgttaaacaccgctt
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 caactaatatattggcaactcaaaaagcattatctggctttgataatact
 aaagttatcctaattgcaggaggtcttgatcgcggtaatgagtttgatga
 attgataccagatatcactggacttaaacatatgggtggttttaggggaat
 cggcatctcgagtaaaacgtgctgcacaaaaagcaggagtaacttatagc
 gatgcttttagatgttagagatgcggtacataaagcttatgaggtggcaca
 acagggcgatggttatcttgctaagtcctgcaaatgcatcatgggacatgt
 ataagaatttcgaagtcctgggtgatgaattcattgatactttcgaaagt
 ctttagaggagag

Table 67: Comparative Sequences relating to SAG0475

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa30176.2{*} April 29, 2002 02:09 ..

	1				50
msa30176.2{305_18RS21}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_2603}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_A909}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_H36B}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_JM9130013}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_COH1}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_M781}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305e_M732}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_090}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_CJB110}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
msa30176.2{305_1169NT}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTT TAGT
Consensus	-----	-----****	*****	*****	*****
	51				100
msa30176.2{305_18RS21}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_2603}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_A909}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_H36B}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_JM9130013}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_COH1}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_M781}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305e_M732}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_090}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_CJB110}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_1169NT}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
Consensus	*****	*****	*****_**	*****	*****
	101				150
msa30176.2{305_18RS21}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_2603}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_A909}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_H36B}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_JM9130013}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_COH1}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_M781}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305e_M732}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_090}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_CJB110}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_1169NT}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
Consensus	*****	*****	*****	*****	*****
	151				200
msa30176.2{305_18RS21}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_2603}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_A909}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_H36B}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_JM9130013}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_COH1}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_M781}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305e_M732}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_090}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_CJB110}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_1169NT}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa30176.2{305_18RS21}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_2603}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_A909}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_H36B}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_JM9130013}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_COH1}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_M781}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305e_M732}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_090}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_CJB110}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
msa30176.2{305_1169NT}	TCCTTTAGAA	TTGTTAGATG	AGGATTTT TG	TTACATGATT	AAAAATCCAG
Consensus	*****	*****	*****	*****	*****
	251				300
msa30176.2{305_18RS21}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_2603}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_A909}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_H36B}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_JM9130013}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_COH1}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_M781}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305e_M732}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_090}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_CJB110}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_1169NT}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
Consensus	*****	*****	*****	*****	*****
301					
msa30176.2{305_18RS21}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_2603}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_A909}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_H36B}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_JM9130013}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_COH1}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_M781}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305e_M732}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_090}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_CJB110}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_1169NT}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATAC	TTAGTTTCAG	AATCTCAGCT
Consensus	*****	*****	*****	*****	*****
351					
msa30176.2{305_18RS21}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_2603}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_A909}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_H36B}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_JM9130013}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_COH1}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_M781}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305e_M732}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_090}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_CJB110}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_1169NT}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
Consensus	*****	*****	*****	*****	*****
401					
msa30176.2{305_18RS21}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_2603}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_A909}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_H36B}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_JM9130013}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_COH1}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_M781}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305e_M732}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_090}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_CJB110}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_1169NT}	CAGAAGTCTT	gAATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
Consensus	*****	-*****	*****	*****	*****
451					
msa30176.2{305_18RS21}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_2603}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_A909}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_H36B}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_JM9130013}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_COH1}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGgATGATA	AAGATAcTCT
msa30176.2{305_M781}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGgATGATA	AAGATAcTCT
msa30176.2{305e_M732}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGgATGATA	AAGATAcTCT
msa30176.2{305_090}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGgATGATA	AAGATAcTCT
msa30176.2{305_CJB110}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGgATGATA	AAGATAcTCT
msa30176.2{305_1169NT}	GGCTTTCCCTG	CTAGTGAAGT	TGTTTCAGGCT	GCGgATGATA	AAGATAcTCT
Consensus	*****	*****	*****	***-*****	*****-***
501					
msa30176.2{305_18RS21}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_2603}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_A909}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_H36B}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_JM9130013}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_COH1}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_M781}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305e_M732}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_090}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_CJB110}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_1169NT}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
Consensus	*****	*****	*****	*****	*****
551					
msa30176.2{305_18RS21}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_2603}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_A909}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_H36B}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_JM9130013}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_COH1}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_M781}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305e_M732}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_090}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_CJB110}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_1169NT}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
Consensus	*****	*****	*****	*****	*****
	601				650
msa30176.2{305_18RS21}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_2603}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_A909}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_H36B}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_JM9130013}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_COH1}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_M781}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305e_M732}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_090}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_CJB110}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_1169NT}	GGGTCTTTTG	AAGATtATGT	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
Consensus	*****	****_*****	*****	*****	*****
	651				700
msa30176.2{305_18RS21}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_2603}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_A909}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_H36B}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_JM9130013}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_COH1}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_M781}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305e_M732}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_090}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_CJB110}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_1169NT}	GTCTTCATCT	GATTTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
Consensus	*****	*****	*****	*****	*****
	701				750
msa30176.2{305_18RS21}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_2603}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_A909}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_H36B}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_JM9130013}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_COH1}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_M781}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305e_M732}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_090}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_CJB110}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_1169NT}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
Consensus	*****	*****	*****	*****	*****
	751				800
msa30176.2{305_18RS21}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_2603}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_A909}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_H36B}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_JM9130013}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_COH1}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_M781}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305e_M732}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_090}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_CJB110}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_1169NT}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
Consensus	*****	*****	*****	*****	*****
	801				850
msa30176.2{305_18RS21}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_2603}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_A909}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_H36B}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_JM9130013}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_COH1}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_M781}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305e_M732}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_090}	GAATATTATG	TtAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_CJB110}	GAATATTATG	TtAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
msa30176.2{305_1169NT}	GAATATTATG	TcAGTAGAtG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAg
Consensus	*****	*_*****-	*****	*****	*****-
	851				900
msa30176.2{305_18RS21}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_2603}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_A909}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_H36B}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_JM9130013}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_COH1}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_M781}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305e_M732}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_090}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_CJB110}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_1169NT}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_2603}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_A909}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_H36B}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_JM9130013}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_COH1}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_M781}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305e_M732}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_090}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_CJB110}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_1169NT}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_2603}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_A909}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_H36B}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAG-
msa30176.2{305_JM9130013}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_COH1}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_M781}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305e_M732}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_090}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_CJB110}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_1169NT}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_2603}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_A909}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_COH1}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_M781}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305e_M732}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_090}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_CJB110}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
msa30176.2{305_1169NT}	caactaatat	attggcaact	caaaaagcat	tatctggctt	tgataatact
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_2603}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_A909}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_COH1}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_M781}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305e_M732}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_090}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_CJB110}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_1169NT}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_2603}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_A909}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_COH1}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_M781}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305e_M732}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_090}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_CJB110}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_1169NT}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_2603}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_A909}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_COH1}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_M781}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305e_M732}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_090}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_CJB110}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_1169NT}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
Consensus	-----	-----	-----	-----	-----
	1201				1250
msa30176.2{305_18RS21}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_2603}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_A909}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_COH1}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_M781}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305e_M732}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_090}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_CJB110}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_1169NT}	aatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
Consensus	-----	-----	-----	-----	-----
	1251				1300
msa30176.2{305_18RS21}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_2603}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_A909}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_COH1}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_M781}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305e_M732}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_090}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_CJB110}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_1169NT}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
Consensus	-----	-----	-----	-----	-----
	1301				1350
msa30176.2{305_18RS21}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_2603}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_A909}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_COH1}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaa--
msa30176.2{305_M781}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305e_M732}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_090}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_CJB110}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_1169NT}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcg-----
Consensus	-----	-----	-----	-----	-----
	1351	1362			
msa30176.2{305_18RS21}	cttagaggag	ag			
msa30176.2{305_2603}	cttagaggag	ag			
msa30176.2{305_A909}	cttagaggag	ag			
msa30176.2{305_H36B}	-----	--			
msa30176.2{305_JM9130013}	cttagaggag	ag			
msa30176.2{305_COH1}	-----	--			
msa30176.2{305_M781}	cttagaggag	ag			
msa30176.2{305e_M732}	cttagaggag	ag			
msa30176.2{305_090}	cttagaggag	ag			
msa30176.2{305_CJB110}	cttagaggag	ag			
msa30176.2{305_1169NT}	-----	--			
Consensus	-----	--			

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVDGKPFDENPTAQSLLLEGIKVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGITGSNGK
TTTTTMI AEVLNAGGQRLLAGNIGFPASEVVQAADDKDILVMELSSFLMGVKEFRPHI
AVITNLMPTHL DYHGSFEDYVAAKWN IQNQMS SDFLVLFNFQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHLRLQSLGKVHGISFYNDKSTN ILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGV TYS DALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVDGKPFDENPTAQSLLLEGIKVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGITGSNGK
TTTTTMI AEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFLMGVKEFRPHI
AVITNLMPTHL DYHGSFEDYVAAKWN IQNQMS SDFLVLFNFQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATIAVAKLAGISNQVIRET
LSNFGGVKHLRLQSLGKVHGISFYNDKSTN ILATQKALSGFDNTKVILIAGGLDRGNEFD

Table 67: Comparative Sequences relating to SAG0475

ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI
KVVCGSHPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI
TGSNGKTTTTTTMIAEVLNAGGQ RGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSK

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI
KVVCGSHPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI
TGSNGKTTTTTTMIAEVLNAGGQ RGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI
KVVCGSHPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI
TGSNGKTTTTTTMIAEVLNAGGQ RGLLAGNIGFPASEVVQAADDKDILVMELSS FQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI
KVVCGSHPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI
TGSNGKTTTTTTMIAEVLNAGGQ RGLLAGNIGFPASEVVQAADDKDILVMELSS FQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFE

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI
KVVCGSHPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI
TGSNGKTTTTTTMIAEVLNAGGQ RGLLAGNIGFPASEVVQAADDKDILVMELSS FQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI
KVVCGSHPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI
TGSNGKTTTTTTMIAEVLNAGGQ RGLLAGNIGFPASEVVQAADDKDILVMELSS FQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEEYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATI AVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPF DENPTAQSLL EEGI KVVCGS
HPLELLDEDFCYMIKNPGI PYNPNPMVKKALEKQIPVLTEVELAYLVSESQ LIGITGSNGK
TTTTT MIAEVLNAGGQ RGLLAGNIGFPASEVVQAADDKDTLVMELSS FQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKE LAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISNQVIRET
LSNFGGVKHLRQLSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGDVILXSP
ANASWDMYKNFEVRGDEFIDTF

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIIVTVNDGKPFDENPTAQSLLLEEGI
 KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMTIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMEISSFQLMGVK
 EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIQNMSSSDFLVNLFNQGISKEKAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETLSNFGGVKHLQSLGKVHGHSFYNDKSTNIIATQKALSGFDNTKVILIAAGGLD
 RSNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIIVTVNDGKPFDENPTAQSLLLEEGI
 KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMTIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMEISSFQLMGVK
 EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIQNMSSSDFLVNLFNQGISKEKAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETLSNFGGVKHLQSLGKVHGHSFYNDKSTNIIATQKALSGFDNTKVILIAAGGLD
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25243.2{*} April 29, 2002 02:20 ..

	1		50
msa25243.2{305_18RS21}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_2603}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_JM9130013}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_COH1}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_M732}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_M781}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_1169NT}	-----ITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_A909}	-----ITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_CJB110}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_090}	-----ITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_H36B}	grvmktITTF	ENKKVLVLGL ARSGEAAARL	LAKLGAIIVTV NDGKPFDENP
Consensus	-----*****	*****	*****
	51		100
msa25243.2{305_18RS21}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_2603}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_JM9130013}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_COH1}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M732}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M781}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_1169NT}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_A909}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_CJB110}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_090}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
msa25243.2{305_H36B}	TAQSLLLEEGI	KVVCGSHPLE LLDEDFCYMI	KNPGIPYNNP MVKKALEKQI
Consensus	*****	*****	*****
	101		150
msa25243.2{305_18RS21}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_2603}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_JM9130013}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_COH1}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M732}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M781}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_1169NT}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_A909}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_CJB110}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_090}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_H36B}	PVLTEVELAY	LVSESQLIGI TGSNGKTTTT	TMIAEVLNAG GQRGLLAGNI
Consensus	*****	*****	*****
	151		200
msa25243.2{305_18RS21}	GFPASEVVQA	AnDKDtlVME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_2603}	GFPASEVVQA	AnDKDtlVME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_JM9130013}	GFPASEVVQA	AnDKDtlVME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_COH1}	GFPASEVVQA	AddKDiLME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M732}	GFPASEVVQA	AddKDiLME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M781}	GFPASEVVQA	AddKDiLME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_1169NT}	GFPASEVVQA	AddKDiLME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_A909}	GFPASEVVQA	AnDKDtlVME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_CJB110}	GFPASEVVQA	AddKDiLME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_090}	GFPASEVVQA	AddKDiLME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_H36B}	GFPASEVVQA	AnDKDtlVME LSSFQLMGVK	EFRPHIAVIT NLMPTHLDYH
Consensus	*****	*-***-*****	*****

Table 67: Comparative Sequences relating to SAG0475

msa25243.2{305_18RS21}	201	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	250	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_2603}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_JM9130013}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_COH1}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_M732}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_M781}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_1169NT}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_A909}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
	msa25243.2{305_CJB110}	GSFEdYVAAK	WNIQNQMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_H36B}	Consensus	****-*****	*****	*****	*****	*****
msa25243.2{305_18RS21}	251	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	300	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_2603}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_JM9130013}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_COH1}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_M732}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_M781}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_1169NT}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_A909}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
	msa25243.2{305_CJB110}	KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN
msa25243.2{305_090}	Consensus	*****	*****	-*****	****-*****	*****
msa25243.2{305_18RS21}	301	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	350	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_2603}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_JM9130013}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_COH1}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_M732}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_M781}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_1169NT}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_A909}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
	msa25243.2{305_CJB110}	QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_090}	Consensus	*****	*****	*****	DSK-----	-----
msa25243.2{305_18RS21}	351	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	400	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_2603}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_JM9130013}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_COH1}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_M732}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_M781}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_1169NT}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_A909}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
	msa25243.2{305_CJB110}	kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_090}	Consensus	-----	-----	-----	-----	-----
msa25243.2{305_18RS21}	401	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	450	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_2603}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_JM9130013}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_COH1}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_M732}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_M781}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_1169NT}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_A909}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
	msa25243.2{305_CJB110}	daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_090}	Consensus	-----	-----	-----	-----	-----
msa25243.2{305_18RS21}	451	lrge				
	msa25243.2{305_2603}	lrge				
	msa25243.2{305_JM9130013}	lrge				
	msa25243.2{305_COH1}	----				
	msa25243.2{305_M732}	lrge				
	msa25243.2{305_M781}	lrge				
	msa25243.2{305_1169NT}	----				
	msa25243.2{305_A909}	lrge				
	msa25243.2{305_CJB110}	lrge				
	msa25243.2{305_090}	lrge				
msa25243.2{305_H36B}	Consensus	----				

Table 68: Comparative Sequences relating to SAG 0499

SEQ ID NO. 6801

STRAIN 2603

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCCTATAAACAGGGACTTTTGTATACACGAGAG
CAAGCGAAACGTGGTGTATGGCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTAT
GATAAACCCAGGTGAAAAGGTTGCAGACGATACTGAATTAATAAAGGTGAAAACTAA
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG
CTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGG
AAGTTACGTCAGGATCATCGTGTTCGTTCTATGGAACAATATAATTTAGGTATGCCAA
AAAGAAGATTTCAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGTAAAAATGGTATTGTCAA
GACAAGTTGGTTTCATGAAAAGGTTTGAACAACAGTGACCAATTTACGAAAGATTATGGA
TATACGGTTAAACATCTTGATTTTTCGCCCATTCAGGTGGACATGGAAATATTGAGTTT
TTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGAT
GTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6802

STRAIN 090

GCTAAAGAGAGGGTAGATGTTCTTGCCCT
ATAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTGGTGTATG
GCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACAGG
TGAAAAGGTTGCAGACGATACTGAATTAATAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCACTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGT
GTTCTGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTT
CAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCATTCAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6803

STRAIN A909

GCTAAAGAGAGGGTAGATGTTCTTGCCCTA
TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACAGGT
GAAAAGGTTGCAGACGATACTGAATTAATAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCACTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTT
AAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATTT
TTTCGCCCATTCAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6804

STRAIN H36B

GCTAAAGAGAGGGTAGATGTTCTTGCCCTATAAACAGG
GACTTTTTGTATACACGAGAGCAAGCGAAACGTGGTGTATGGCAGGAATG
GTGATTAACGTTATCAATGGAGAACGTTATGATAAACAGGTGAAAAGGT
TGCAGACGATACTGAATTAATAAAGGTGAAAACTAAAATATGTTA
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAG
GAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTGTTCGTTCT
ATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTCAAGGAGGG
ACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCTTAATTTGA
TTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGTAAAAATGG
TATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAACAGTGACCA
ATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC
ATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTGCAAAAGTG
TCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGTTATAGAAA
AAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6805

STRAIN 18RS21

GCTAAAGAGAGGGTAGATGTTCTTGCCCTA
TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACAGGT

Table 68: Comparative Sequences relating to SAG 0499

GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTGAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTT
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTGCTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6806

STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGACTGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGC
 GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTGAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTT
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTGCTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6807

STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
 GCAGGACTGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGG
 CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
 GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
 TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTGAGGATCATCGT
 GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
 CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAACCACAATTTGAAGCAGGTGCTGAGCAAATTGG
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTGGACAA
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
 TTTTCGCCCCTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
 GCAAAAGTGTCAAGATCCACAAAATCTTGCTTGACCAAATACAAGATG
 TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6808

STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
 GCAGGACTGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGG
 CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
 GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
 TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTGAGGATCATCGT
 GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
 CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAACCACAATTTGAAGCAGGTGCTGAGCAAATTGG
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTGGACAA
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
 TTTTCGCCCCTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
 GCAAAAGTGTCAAGATCCACAAAATCTTGCTTGACCAAATACAAGATG
 TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6809

STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGT
 GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT

Table 68: Comparative Sequences relating to SAG 0499

GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGACTGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGC
 GAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGGT
 GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
 TAATTTGATTTTGCCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGT
 GAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGGT
 GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

PRETTY of: /biotmp/msa236683.2{*} May 14, 2003 02:57 ..

	1		50
msa236683.2{310_090}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_18RS21}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_2603}	atgGCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_A909}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_CJB110}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_H36B}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_JM9130013}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_COH1}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_M732}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_M781}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
msa236683.2{310_1169NT}	---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA		
Consensus	*****	*****	*****
	51		100
msa236683.2{310_090}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_18RS21}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_2603}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_A909}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_CJB110}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_H36B}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_JM9130013}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_COH1}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_M732}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_M781}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
msa236683.2{310_1169NT}	TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAAACG		
Consensus	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

msa236683.2{310_090}	101	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	150	TGCAGACGAT
msa236683.2{310_18RS21}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT		
msa236683.2{310_2603}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT		
msa236683.2{310_A909}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT		
msa236683.2{310_CJB110}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT		
msa236683.2{310_H36B}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT		
msa236683.2{310_JM9130013}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT		
msa236683.2{310_COH1}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT		
msa236683.2{310_M732}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT		
msa236683.2{310_M781}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT		
msa236683.2{310_1169NT}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT		
Consensus	*****	*****	*****	*-*****	*****		
msa236683.2{310_090}	151	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	200	GTAGAGGTGG
msa236683.2{310_18RS21}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_2603}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_A909}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_CJB110}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_H36B}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_JM9130013}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_COH1}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_M732}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_M781}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
msa236683.2{310_1169NT}	ACTGAATTAA	AACTAAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG		
Consensus	*****	*****	*****	*****	*****		
msa236683.2{310_090}	201	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	250	GTTGCAGATA
msa236683.2{310_18RS21}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_2603}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_A909}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_CJB110}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_H36B}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_JM9130013}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_COH1}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_M732}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_M781}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
msa236683.2{310_1169NT}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA		
Consensus	*****	*****	*****	*****	*****		
msa236683.2{310_090}	251	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	300	TGATGTTATG
msa236683.2{310_18RS21}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_2603}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_A909}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_CJB110}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_H36B}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_JM9130013}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_COH1}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_M732}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_M781}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
msa236683.2{310_1169NT}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTTAC	TGATGTTATG		
Consensus	*****	*****	*****	*****	*****		
msa236683.2{310_090}	301	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	350	GAACAAATCA
msa236683.2{310_18RS21}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_2603}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_A909}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_CJB110}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_H36B}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_JM9130013}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_COH1}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_M732}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_M781}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
msa236683.2{310_1169NT}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA		
Consensus	*****	*****	*****	*****	*****		
msa236683.2{310_090}	351	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	400	ATGGAACAAT
msa236683.2{310_18RS21}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_2603}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_A909}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_CJB110}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_H36B}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_JM9130013}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_COH1}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_M732}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_M781}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
msa236683.2{310_1169NT}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTTCGTTCT	ATGGAACAAT		
Consensus	*****	*****	*****	*****	*****		

Table 68: Comparative Sequences relating to SAG 0499

msa236683.2{310_090}	401	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	450
msa236683.2{310_18RS21}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_2603}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_A909}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_CJB110}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_H36B}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_JM9130013}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_COH1}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_M732}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_M781}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
msa236683.2{310_1169NT}		ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA	
Consensus		*****	*****	*****	*****	*****	
msa236683.2{310_090}	451	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	500
msa236683.2{310_18RS21}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_2603}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_A909}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_CJB110}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_H36B}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_JM9130013}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_COH1}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_M732}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_M781}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTaCCAGC	
msa236683.2{310_1169NT}		TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTTGA	TTTTgCCAGC	
Consensus		*****	*****	*****	*****	*****	
msa236683.2{310_090}	501	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	550
msa236683.2{310_18RS21}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_2603}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_A909}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_CJB110}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_H36B}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_JM9130013}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_COH1}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_M732}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_M781}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
msa236683.2{310_1169NT}		TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC	
Consensus		*****	*****	*****	*****	*****	
msa236683.2{310_090}	551	CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	600
msa236683.2{310_18RS21}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_2603}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_A909}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_CJB110}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_H36B}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_JM9130013}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_COH1}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_M732}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_M781}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
msa236683.2{310_1169NT}		CACAATTTGA	AGCAGGTCGT	GAGCAAATTG	GTAAAAATGG	TATTGTCAAA	
Consensus		*****	*****	*****	*****	*****	
msa236683.2{310_090}	601	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	650
msa236683.2{310_18RS21}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_2603}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_A909}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_CJB110}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_H36B}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_JM9130013}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_COH1}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_M732}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_M781}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
msa236683.2{310_1169NT}		GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACAGAA	
Consensus		*****	*****	*****	*****	*****	
msa236683.2{310_090}	651	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	700
msa236683.2{310_18RS21}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	
msa236683.2{310_2603}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	
msa236683.2{310_A909}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	
msa236683.2{310_CJB110}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	
msa236683.2{310_H36B}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	
msa236683.2{310_JM9130013}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	
msa236683.2{310_COH1}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	gTTCAAGGTG	
msa236683.2{310_M732}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	gTTCAAGGTG	
msa236683.2{310_M781}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	gTTCAAGGTG	
msa236683.2{310_1169NT}		AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG	

Table 68: Comparative Sequences relating to SAG 0499

Consensus	*****	*****	*****	*****	*****
	701				750
msa236683.2{310_090}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_18RS21}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_2603}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_A909}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_CJB110}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_H36B}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_JM9130013}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_COH1}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_M732}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_M781}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
msa236683.2{310_1169NT}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa236683.2{310_090}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_18RS21}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_2603}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_A909}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_CJB110}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_H36B}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_JM9130013}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_COH1}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_M732}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_M781}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_1169NT}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
Consensus	*****	*****	*****	*****	*****
	801				825
msa236683.2{310_090}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_18RS21}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_2603}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_A909}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_CJB110}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_H36B}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_JM9130013}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_COH1}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_M732}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_M781}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_1169NT}	GGAATTTAAG	AAAAATGAAG	AAGAG		
Consensus	*****	*****	*****		

SEQ ID NO. 6812

STRAIN 2603 frame: 1

MAKERVVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLGKGLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGNTQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6813

STRAIN 090 frame: 1

AKERVVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLGKGLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGNTQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6814

STRAIN A909 frame: 1

AKERVVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLGKGLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGNTQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6815

STRAIN 18RS21 frame: 1

AKERVVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLGKGLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGNTQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6816

STRAIN M732 frame: 1

AKERVVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLGKGLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGNTQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL

Table 68: Comparative Sequences relating to SAG 0499

IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821

STRAIN JM9130013 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

PRETTY of: /biotmp/msa236800.2{*} May 14, 2003 02:58 ..

	1		50
msa236800.2{310_090}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_18RS21}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_2603}	MAKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_A909}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_CJB110}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_H36B}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_JM9130013}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_COH1}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M732}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M781}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_1169NT}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
Consensus	*****	*****	*****

	51		100
msa236800.2{310_090}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_18RS21}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_2603}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_A909}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_CJB110}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_H36B}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_JM9130013}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_COH1}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M732}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M781}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_1169NT}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
Consensus	*****	*****	*****

101

150

Table 68: Comparative Sequences relating to SAG 0499

msa236800.2{310_090}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_18RS21}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_2603}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_A909}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_CJB110}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_H36B}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_JM9130013}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_COH1}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_M732}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_M781}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
msa236800.2{310_1169NT}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFK EGLPE
Consensus	*****	*****	*****	*****	*****
151					
msa236800.2{310_090}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_18RS21}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_2603}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_A909}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_CJB110}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_H36B}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_JM9130013}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_COH1}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M732}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M781}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_1169NT}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
Consensus	*****	*****	*****	*****	*****
201					
msa236800.2{310_090}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_18RS21}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_2603}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_A909}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_CJB110}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_H36B}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_JM9130013}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_COH1}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M732}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M781}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_1169NT}	DKLVHEKVLT	TVTNFTKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
Consensus	*****	*****	*****	-*****	*****
251					
msa236800.2{310_090}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_18RS21}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_2603}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_A909}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_CJB110}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_H36B}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_JM9130013}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_COH1}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M732}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M781}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_1169NT}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
Consensus	*****	*****	*****		
275					

Table 69: Comparative Sequences relating to SAG0032

SEQ ID NO. 6901

STRAIN 2603

ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT
 GTTCAAGCACAAGAAACAGATACGACGTGGACAGCACGTACTGTTTCAGAGGTAAAGGCT
 GATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC
 GTTATTTTCAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA
 GATATCAATCTTATTTATCTCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCAT
 ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCT
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACA
 ATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAGACATAT
 TCTTCTGCGCCAGCTTTGAAATCAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA
 GCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCA
 GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACT
 GTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCTAAAGTAGAACTGGTGCA
 TCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGACTACGACTTCACCAGCTACAGAC
 AGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCA
 ACACCGGTAGCACAAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
 GGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT
 GAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC
 TTTATTGTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAAT
 ATGGCAGCAAATAACATTTTATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAAC
 AGTATTTATGGACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCCTATGACCAGTTTACGTATCATTTAACAATAATATAAAAAAGGAAGCTATTTG
 GCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATTA

SEQ ID NO. 6902

STRAIN 090

TGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTT
 CAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCT
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTC
 TCTCAATACAATTTTGGGAAGGTATGACACCAGAAGCAGCAACAACGATTG
 TTTCCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAGAA
 GTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGT
 ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG
 AGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC
 GGTAAGAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTC
 CTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTT
 CCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGA
 AGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAG
 CACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
 GGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTA
 TGGAGTTAATGAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATG
 GTAAAGGTTTAGCAGTCGACTTTATTGTAGGTAAAAACCAAGCACTTGGT
 AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTT
 ATATGTTATCTGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATG
 GACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCATTATGACCAGTTTACGTATCATTTAACAATAATATAAAAAAGG
 AAGCTATTTGGCTTCTTTTTATATGCCTTGAATAGACTTTCAAGGTTCT
 TATATAATTTTTATTA

SEQ ID NO. 6903

STRAIN A909

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA
 ATATGGTGATACACTAAGCGTTATTTTCAAGCAATGTCAATTGATATGA
 ATGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCT
 GAGACAACACTGaCAGTAACTTACGATCAGAAGAGTCATACTGCTACTTC
 AATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAaCAGcTA
 CTGTGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCT
 CTCAATACAATTTTGGGAAGGTATGACACCAGAAGCAGCAACAACGATTGT
 TTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAGAAG
 TATTAgCACAAGGGCaAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTA
 TCACcAGCTcCTGTGAAGTCGATTACTTCAGAAGTTCCAgCAGCTAAAGA
 GGAAGTTAAACCAaCTCagACGTCAgTCAGTCAGTCAACAACAGTATCAC
 CAgCTTCTGTTGCCGCTGAAACACCAGCTCCAgTAGCTAAaGTAGCACCG
 GTAAGAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCC
 TAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTC
 CTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAA
 GTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGC
 ACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAA
 GGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTAT
 GGAGTTAATGAATTcAGTACATACCGTGCGGGAGATCCAGGTGATCATGG
 TAAAGGTTTAGCAGTTGACTTTATTGTAgGTAAAAACCAAGCACTTGGTA
 ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCaAATAACATTTCA
 TATGTTATCTGGCAACAAAAGTTTTACTCAAATaCAAATAGTATTTATGG
 ACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTAcTGCCA
 ACCaCTATGACCAGTTTACGTATCATTTAACAATAATATAAAAAAGGA
 AGCTaTTTGGCTTCTTTTTATATGCCTTGCATAGACTTCAAGGTTCTT
 ATATAATTTTTATTA

SEQ ID NO. 6904

STRAIN H36B

Table 69: Comparative Sequences relating to SAG0032

CTGATTTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA
 TGGTGATACAcTAAGCGTTATTTTCAGAAGCAATGTCaATTGATATGAATG
 TCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAG
 ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT
 GAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTG
 TCGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTC
 AATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTC
 GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAAGAAGTAT
 TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCA
 CCAGCTCCTGTGAAGTCGATTACTTTCAGAAGTTCCAGCAGCTAAAGAGGA
 AGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACCAG
 CTTCTGTTGCGCTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACCAGGTA
 AGAAGCTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCTCTAA
 AGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTCTG
 TGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAAGTT
 AAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACA
 ACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAAGGC
 TCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGA
 GTTAATGAATTCAGTACATACCGTGCAGGAGATCCAGGTGATCATGGTAA
 AGGTTTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATG
 AAGTTGCACAGTACTCTACACAAAATaTGGCAGCAAATAACATTTTCATAT
 GTTATCTGGCaACAAAAGTTTACTCAAATACAAATAGTATTTATGGACC
 TGCTAATACTTGGAAATGCAATGCCaATCGTGGTGGCGTTACTGCCAACC
 ACTATGACCAGTTTACGTATCATTTAACAAATAATATAAAAAAGGAAGC
 TATTTGGCTTCTTTTATATATGCTTGCATAGACCTTCAAGGTTCTTATA
 TAATTTTTTATTA

SEQ ID NO. 6905

STRAIN 18RS21

CTGATTTGGTAAAGCAAGACAAT

AAATCATCATATACTGTGAAATATGGTGATACAcTAAGcGTTATTTTCAGA
 AGCAATGTCAATTGATATGAATGTCTTAGCAAAAaTAAATAACATTGCAG
 ATATCAATCTTATTTATCCTGAGACAACaCTGaCAGTAaCTTACGATCAG
 AAGAGTCATACTGCCaCTTCAATGAAAATAGAAAACACCAGCAaCAAATGC
 TGCTGGTCAaACaCAGCTACTGTGGATTGAAAACCAATCAaGTTTCTG
 TTGCAGACCAAAAAGTTTCTCTCAATACAATTTTCGGAAGGTATGACACCA
 GAAGCAGCAACAACGATTGTTTCGCCAATGAAGACaTATTCTTCTGCGCC
 AGCTTTGAAaTCAAAAAGAAGTATTAGCACAAAGAGCAAGCTGTTAGTCAAG
 CAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCA
 GAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG
 TCAGTCAACAACAGTATCACCAGCTTCTGTTGCCGCTGAAAACACCAGCTC
 CAGTAGCTAAAGTAGCACCGGTAAGAACTGTAGCAGCCCCCTAGAGTGGCA
 AGTGTAAAGTAGTCACTCCTAAAGTAGAACTGGTGATCACCAGAGCA
 TGTATCAGCTCCAGCAGTTCTGTGACTACGACTTCAACAGCTACAGACA
 GTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCT
 CCAACAGCAACACCGGTAGCACAAACAGCTTCAACAACAAATGCAGTAGC
 TGCACATCCTGAAAATGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAG
 AAAAGTAGCGTCAACTTATGGAGTTAATGAATTCACTACATACCGTGGC
 GGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGG
 TACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAATA
 TGGCAGCAAATAACATTTTCATATGTTATCTGGCAACAAAAGTTTACTCA
 AATACAAACAGTATTTATGGACCTGCTAATACTTGAATGCAATGCCAGA
 TCGTGGTGGCGTTACTGCCAACCCTATGACCACGTTACGTATCATTTA
 ACAATAATATAAAAAAGGAAGCTATTTGGCTTCTTTTATATATGCTTG
 AATAGACTTTCAAGGTTCTTATATAATTTTTTATTA

SEQ ID NO. 6906

STRAIN COH1

CTGATTT

GGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACAC
 TAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAA
 ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGAC
 AGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAA
 CACCAGCAACAAATGCTGCTGGTCAAACAACAGcTACTGTGATTTGAAA
 ACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACAATTT
 GGAAGGTATGACACCAGaAGCAGCAACAACGATTGTTTCGCCAATGAAGA
 CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAAGAAGTATTAGCACAAAG
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT
 GAAGTCGATTACTTCAAGGTTCCAGCAGCTAAAGAGGAAGTTAAACCAA
 CTCAGACGTCAGTCAGTCACTTAAACAACAGTATCACCAGCTTCTGTTGCC
 GCTGAAAACACCAGCTCCAGTAGCTAAAAGTAGCACCGGTAAGAACTGTAGC
 AGCCCCCTAGAGTGGCAAGTGCTAAAAGTAGTCACTCTTAAAGTAGAACTG
 GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGACTACGACT
 TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC
 GGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACAGCTTCAA
 CAACAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTCAT
 GTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAATT
 CAGTACATACCGTGCAGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAG
 TTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACAG
 TaCTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATCTGGCA
 ACAAAAAGTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTT
 GGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCCTATGACCAC
 GTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTGGCTTC

Table 69: Comparative Sequences relating to SAG0032

TTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT
A

SEQ ID NO. 6907

STRAIN M732

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACAnTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
CACTGACAGTAACTTACGATCAGAAGAGTCAtACTGCCACTTCAATGAAA
ATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGAAAACCAATCAAGTTTTTGTTCAGACCAAAAAGTTTTCTCTCAATA
CAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTTCGCCA
ATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTCGATTACTTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCAACTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTC
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC
TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAaCACCGGTAGCACAACCA
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTCAAGTACATACCGTGCAGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTTAttgtaggtaaaaaccaAGCACTTGGTAATGAAGT
TGCACAGTACTcTACACAAAATATGGCAGCAAATAACATTTTATATGTTA
TCTGGCAACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCT
AATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCACGTTACAGTATCATTTAACAATAATATAAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6908

STRAIN M781

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
CACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
ATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGAAAACCAATCAAGTTTTTGTTCAGACCAAAAAGTTTTCTCTCAATA
CAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTTCGCCA
ATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTCGATTACTTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCAACTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTC
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC
TACGACTTCACCAGCTACAGACAGTaaGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAACCA
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTCAAGTACATACCGTGCAGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGT
TGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTATATGTTA
TCTGGCAACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCT
AATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCACGTTACAGTATCATTTAACAATAATATAAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA
TATGGTGATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAA
TGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTG
AGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTTCA
ATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCTAC
TGTTGGATTTGAAAACCAATCAAGTTTcTGTTGCAGACCAAAAAGTTTTCTC
TCAATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT
TCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGT
ATTAGCACAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTAT
CAACAGCTCCTGTGAAGTCGATTACTTTCAGAAGTTCCAGCAGCTAAAGAG
GAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC
AgCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGG
TAAgAACTGTAGCAGCCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCT
AAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCC
TGTGACTACGACTTCAACAGcTACAGACAGTaAGTTaCAAGCGACTGAAG
TTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCA
CAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGG
GCTCCAACCTCATGTTGCAGCTTATaAAGAAAAAGTAGCGTCAACTTATG
GAGTTAATGAATTCAAGTACATaCCGTGCAGGTGATCCAgGTGATCATGGT
AAAGGTTTAGCAGTcGACTTTATTGTAGTAAAAACCAAGCACTTGGTAA

Table 69: Comparative Sequences relating to SAG0032

TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCAT
ATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGA
CCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA
CCATTATGACCATGTTACAGTATCATTTAACAAATAATATAAAAAAGGAA
GCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGGTTCTTA
TATAATTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT

CTGATTTG

GTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT
AAGCGTTATTTTCAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAA
TTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGACA
GTAACTTACGATCAGAAAGAGTCATACTGCCACTTCAATGAAAATAGAAAC
ACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTGGATTTGAAAA
CCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACAATTTTCG
GAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAGAC
ATATTCCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAGC
AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTG
AAGTCGATTACTTTCAGAAAGTTCAGCAGCTAAAGAGGAAGTTAGACCAaC
TcAGACGTCAGTCAGTCAGTCAACAACAGTATCACCAGCTTCTGTTGCCG
CTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACTGTAGCA
GCCCCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTAGA
AAcTGGTGCATCACCAGAGCATGTACCAGCTCCAGCAGTTcCTGTGACTA
cGACTTCAACAGCTACaGACaTaAGTTACAAGCGACTGAAGTTAAgAGC
GtTCCGGTgGCACAAAAAGCTCCAACAGCAACACCGGTaGCACAACCAGC
TTcAAACAACAATGCAGTAGcTGCACATCTGAAAATGCAGGACTCCAAC
CTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCACTTATGGAGTTAAT
GAATTCAGTACATaCCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTT
AGCAGTTGACTTTATTGTaGTA AAAACCAAGCACTTGGTAATGAAGTTG
CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTATATGTTATC
TGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA
TACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG
ACCAGGTTACAGTATCATTTAACAATAATATAAAAAAGGAAGCTATTTG
GCTTCTTTTATATGCCTTGAATAGACTTTCAAGGtTCTTATATAATTT
TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT

GTGAAATATGGTGATACACTAAGCGTTATTTTCAAGCAATGTCAATTGA
TATGAATGTCTTAGCAAAAAATAAATAACATTGCAGATATCAATCTTATTT
ATCCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCC
ACTTCAATGAAAATAGAAACACCAGCAACAATGCTGCTGGTCAAACAAC
AGCTACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAG
TTTCTCTCAATACAATTTTGGAAAGGTATGACACCAGAAGCAGCAACAACG
ATTGTTTTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAA
AGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAAC
AGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAAGGTTCCAGCAGCT
AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGT
ATCACCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAG
CACCGGTAAGAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTC
ACTCCTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGC
AGTTCTGTGACTACGACTTACCAGCTACAGaCAGTAAGTTACAAGCGA
cTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCG
GTAGCaCAACCAGCTTCAACAACAATGCAGTAGCTGCACATCTGAAAA
TGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAA
CTTATGGAGTTAATGAATTCAGTACATACCGTGCAGGAGATCCAGGTGAT
CATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGGTACTAATCAAGCACT
TGGTAATAAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACA
TTTCATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAACAGTATT
TATGGACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTAC
TGCCAACCACTATGACCAGTTACAGTATCATTTAACAATAATATAAAAA
AAGGAAGCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTTCAAGG
TTCTTATATAATTTTATTA

PRETTY of: /biotmp/msa167919.2{*} March 11, 2003 08:55 ..

	1				50
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	atgaataaaa	aggatatt	gacatcgaca	atggcagctt	cgctattatc
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

51

100

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	agtcgcaagt	gttcaagcac	aagaaacaga	tacgacgtgg	acagcacgta
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
101					
msa167919.2{322_COH1}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_M781}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_M732}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_18RS21}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_2603}	ctgtttcaga	ggtaaaggct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_JM9130013}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_A909}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_H36B}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_1169NT}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
Consensus	*****	*****	-----	-----	-----
151					
msa167919.2{322_COH1}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M781}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M732}	tatactgtga	aatatgggtga	tacantaagc	gttatttcag	aagcaatgtc
msa167919.2{322_18RS21}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_2603}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_JM9130013}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_A909}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_H36B}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_1169NT}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
Consensus	-----	-----	-----	-----	-----
201					
msa167919.2{322_COH1}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M781}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M732}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_18RS21}	aattgatatg	aatgtcttag	caaaaataaa	taacattgca	gatatcaatc
msa167919.2{322_2603}	aattgatatg	aatgtcttag	caaaaataaa	taacattgca	gatatcaatc
msa167919.2{322_JM9130013}	aattgatatg	aatgtcttag	caaaaataaa	taacattgca	gatatcaatc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_A909}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_H36B}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_1169NT}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
Consensus	-----	-----	-----	-----	-----
251					
msa167919.2{322_COH1}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M781}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M732}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_18RS21}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_2603}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_JM9130013}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_090}	-----	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_CJB110}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_A909}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_H36B}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_1169NT}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
Consensus	-----	*****	*****	*****	*****
301					
msa167919.2{322_COH1}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M781}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M732}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_18RS21}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_2603}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_JM9130013}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_090}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_CJB110}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_A909}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_H36B}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_1169NT}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
Consensus	*****	*****	*****	*****	*****
350					

Table 69: Comparative Sequences relating to SAG0032

	351				400
msa167919.2{322_COH1}	AACAaCAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_M781}	AACAaCAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_M732}	AACAaCAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_18RS21}	AACAaCAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_2603}	AACAaCAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_JM9130013}	AACAaCAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_090}	AACAcCAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_CJB110}	AACAcCAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_A909}	AACAaCAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_H36B}	AACAaCAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_1169NT}	AACAaCAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
Consensus	****-*****	*****-****	*****-****	*****-****	*****-****
	401				450
msa167919.2{322_COH1}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_M781}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_M732}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_18RS21}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_2603}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_JM9130013}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_090}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_CJB110}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_A909}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_H36B}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_1169NT}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
Consensus	*****-****	*****-****	*****-****	*****-****	*****-****
	451				500
msa167919.2{322_COH1}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_M781}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_M732}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_18RS21}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_2603}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_JM9130013}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_090}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_CJB110}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_A909}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_H36B}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_1169NT}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
Consensus	*****-****	*****-****	*****-****	*****-****	*****-****
	501				550
msa167919.2{322_COH1}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GtAGCAGCTA
msa167919.2{322_M781}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GtAGCAGCTA
msa167919.2{322_M732}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GtAGCAGCTA
msa167919.2{322_18RS21}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_2603}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_JM9130013}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_090}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_CJB110}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_A909}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_H36B}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_1169NT}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
Consensus	*****-****	*****-****	***-*****	*****-****	*-*****
	551				600
msa167919.2{322_COH1}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_M781}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_M732}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_18RS21}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_2603}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_JM9130013}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_090}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_CJB110}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_A909}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_H36B}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_1169NT}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
Consensus	*****-****	*****-****	*****-****	*****-****	*****-****
	601				650
msa167919.2{322_COH1}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTtAAC
msa167919.2{322_M781}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTtAAC
msa167919.2{322_M732}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTtAAC
msa167919.2{322_18RS21}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_2603}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_JM9130013}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_090}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_CJB110}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_A909}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_H36B}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_1169NT}	GCAGCTAAAG	AGGAAGTTAg	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
Consensus	*****-****	*****-****	*****-****	*****-****	*****-****

Table 69: Comparative Sequences relating to SAG0032

	651				700
msa167919.2{322_COH1}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M781}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M732}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_18RS21}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_2603}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_JM9130013}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_090}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_CJB110}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_A909}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_H36B}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_1169NT}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa167919.2{322_COH1}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M781}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M732}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_18RS21}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_2603}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_JM9130013}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_090}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_CJB110}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_A909}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_H36B}	AAGTAGCACC	GGTAAGAACT	G TAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_1169NT}	AAGTAGCACC	GGTAAGAACT	G TAGcagccc	CAGCCCCTAG	AGTGGCAAGT
Consensus	*****	*****	*****	*****	*****
	751				800
msa167919.2{322_COH1}	GcTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M781}	GcTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M732}	GcTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_18RS21}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_2603}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_JM9130013}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_090}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_CJB110}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_A909}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_H36B}	GtTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_1169NT}	GcTAAAGTAG	TCACTCCTAA	AGTAGAACT	GGTGCATCAC	CAGAGCATGT
Consensus	*-*****	*****	*****	*****	*****
	801				850
msa167919.2{322_COH1}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M781}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M732}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_18RS21}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_2603}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_JM9130013}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_090}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_CJB110}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_A909}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_H36B}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_1169NT}	AcCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAaTA
Consensus	*-*****	*****	*****	*****	*****
	851				900
msa167919.2{322_COH1}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M781}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M732}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_18RS21}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_2603}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_JM9130013}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_090}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_CJB110}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_A909}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_H36B}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_1169NT}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTgGCACA	AAAAGCTCCA
Consensus	*****	*****	*****	*****	*****
	901				950
msa167919.2{322_COH1}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M781}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M732}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_18RS21}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_2603}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_JM9130013}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_090}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_CJB110}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_A909}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_H36B}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_1169NT}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC

Table 69: Comparative Sequences relating to SAG0032

Consensus	*****	*****	*****	*****	*****
	951				1000
msa167919.2{322_COH1}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M781}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M732}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_18RS21}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_2603}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_JM9130013}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_090}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_CJB110}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_A909}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_H36B}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_1169NT}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
Consensus	*****	*****-*-*	*****	*****	*****
	1001				1050
msa167919.2{322_COH1}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_M781}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_M732}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_18RS21}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_2603}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_JM9130013}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_090}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGt
msa167919.2{322_CJB110}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGt
msa167919.2{322_A909}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_H36B}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
msa167919.2{322_1169NT}	AAGTAGCGTC	AACCTTATGGA	GTAAATGAAT	TCAGTACATA	CCGTGCgGGa
Consensus	*****	*****	*****	*****	*****-*-*
	1051				1100
msa167919.2{322_COH1}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M781}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M732}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_18RS21}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_2603}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_JM9130013}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_090}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_CJB110}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_A909}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_H36B}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_1169NT}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
Consensus	*****	*****	*****	**-*****	*****
	1101				1150
msa167919.2{322_COH1}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M781}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M732}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_18RS21}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_2603}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_JM9130013}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_090}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_CJB110}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_A909}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_H36B}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_1169NT}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
Consensus	-*-*****	*****	*****	*****	*****
	1151				1200
msa167919.2{322_COH1}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAtTCAAAT
msa167919.2{322_M781}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAtTCAAAT
msa167919.2{322_M732}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAtTCAAAT
msa167919.2{322_18RS21}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_2603}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_JM9130013}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_090}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_CJB110}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_A909}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_H36B}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_1169NT}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
Consensus	*****	*****	*****	*****	***-*****
	1201				1250
msa167919.2{322_COH1}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M781}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M732}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_18RS21}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_2603}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_JM9130013}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_090}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_CJB110}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_A909}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_H36B}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_1169NT}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
Consensus	*****-****	*****	*****	*****	*****
	1251				1300
msa167919.2{322_COH1}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_M781}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_M732}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_18RS21}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_2603}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_JM9130013}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_090}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msa167919.2{322_CJB110}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msa167919.2{322_A909}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_H36B}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_1169NT}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
Consensus	*****	*****	*-*****	-*****	*****
	1301				1350
msa167919.2{322_COH1}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_M781}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_M732}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_18RS21}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_2603}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_JM9130013}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_090}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_CJB110}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_A909}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_H36B}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msa167919.2{322_1169NT}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
Consensus	*****	*****	*****	*****	*****-*
	1351				1382
msa167919.2{322_COH1}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_M781}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_M732}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_18RS21}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_2603}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_JM9130013}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_090}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_CJB110}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_A909}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_H36B}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
msa167919.2{322_1169NT}	AGACTTTCAA	GGTTCTTATA	TAATTTTTAT	TA	
Consensus	*****	*****	*****	**	

SEQ ID NO. 6912

STRAIN 2603 frame: 1

MNKKVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSSYTVKYGDTLS
 VISEAMSIDMNV LAKINNIADINLIYPETTLTVTYDQKSHTATSMKIETPATNAAGQTTA
 TVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTYSSAPALKSKEVLAQEQA VSQ
 AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETPAPVAKVAPVRT
 VAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVQA KAPTA
 TPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD
 FIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYNSNTINSIYGPANTWNAMPDRGGVTA
 NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6913

STRAIN 090 frame: 2

ETTLTVTYDQKSHTATSMKIETPATNAAGQTPATVDLKTNQVSVADQKVS LNTISEGMTPE
 EAATTIVSPMKTYSSAPALKSKEVLAQEQA VSQAAANEQVSTAPVKSITSEVPAAKEEVK
 PTQTSVSQSTTVSPASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVS
 PAVPVTTTSTATDSKLQATEVKSVPVQA KAPTATPVAQPASTTNAAHPENAGLQPHVA
 AYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS
 YVIWQKQFYNSNTINSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL
 NRLSRFLYNFY

SEQ ID NO. 6914

STRAIN A909 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNV LAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTY
 SSAPALKSKEVLAQQA VSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPVQA KAPTATPVAQPASTTNAAHPENARLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYNSNT
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY

SEQ ID NO. 6915

STRAIN H36B frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNV LAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTY
 SSAPALKSKEVLAQQA VSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPVQA KAPTATPVAQPASTTNAAHPENARLQPHVAAYKEKVASTYGVN

Table 69: Comparative Sequences relating to SAG0032

EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVTPKVTGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTXSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVTPKVTGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVTPKVTGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVTPKVTGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTPATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVTPKVTGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6921

STRAIN 1169NT frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVTPKVTGASPEHVSAPAVPVTTTSTA
TDNKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
VNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQQKFYSN
TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKEINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVTPKVTGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

PRETTY of: /biotmp/msa237049.2{*} May 14, 2003 03:04 ..

	1		50
msa237049.2{322_COH1}	-----	-----	dlvkqdnkss
msa237049.2{322_M781}	-----	-----	dlvkqdnkss
msa237049.2{322_M732}	-----	-----	dlvkqdnkss
msa237049.2{322_A909}	-----	-----	dlvkqdnkss
msa237049.2{322_H36B}	-----	-----	dlvkqdnkss
msa237049.2{322_090}	-----	-----	-----

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_CJB110}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_18RS21}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_2603}	mnkkvlltst	maasllsvas	vqagetdttw	tartvsevka	dlvkqdnkss
msa237049.2{322_JM9130013}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_1169NT}	-----	-----	-----	-----	dlvkqdnkss
Consensus	*****	*****	*****	*****	-----
51					100
msa237049.2{322_COH1}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M781}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M732}	ytvkygdtxs	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_A909}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_H36B}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_090}	-----	-----	-----	-----ETT	LTVTYDQKSH
msa237049.2{322_CJB110}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_18RS21}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_2603}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_JM9130013}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_1169NT}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
Consensus	-----	-----	-----	-----	*****
101					150
msa237049.2{322_COH1}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVf	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_M781}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVf	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_M732}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVf	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_A909}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_H36B}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_090}	TATSMKIETP	ATNAAGQTpa	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_CJB110}	TATSMKIETP	ATNAAGQTpa	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_18RS21}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_2603}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_JM9130013}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
msa237049.2{322_1169NT}	TATSMKIETP	ATNAAGQTta	TVDLKTNQVs	VADQKVSLNT	ISEGMTPEAA
Consensus	*****	*****	*****	*****	*****
151					200
msa237049.2{322_COH1}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpa	PVKsITSEVP
msa237049.2{322_M781}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpa	PVKsITSEVP
msa237049.2{322_M732}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpa	PVKsITSEVP
msa237049.2{322_A909}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	aaANEQVSpa	PVKsITSEVP
msa237049.2{322_H36B}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	aaANEQVSpa	PVKsITSEVP
msa237049.2{322_090}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	aaANEQVSta	PVKsITSEVP
msa237049.2{322_CJB110}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	aaANEQVSta	PVKsITSEVP
msa237049.2{322_18RS21}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	aaANEQVSpa	PVKsITSEVP
msa237049.2{322_2603}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	aaANEQVSpa	PVKsITSEVP
msa237049.2{322_JM9130013}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	aaANEQVSpa	PVKsITSEVP
msa237049.2{322_1169NT}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	aaANEQVSpa	PVKsITSEVP
Consensus	*****	*****	*****	*****	*****
201					250
msa237049.2{322_COH1}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M781}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M732}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_A909}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_H36B}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_090}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_CJB110}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_18RS21}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_2603}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_JM9130013}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_1169NT}	AAKEEVrPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VAapAPRVAS
Consensus	*****	*****	*****	*****	*****
251					300
msa237049.2{322_COH1}	aKVVTpKVET	GASPEHVsAP	AVPVTtTSpA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_M781}	aKVVTpKVET	GASPEHVsAP	AVPVTtTSpA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_M732}	aKVVTpKVET	GASPEHVsAP	AVPVTtTSpA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_A909}	vKVVTpKVET	GASPEHVsAP	AVPVTtTStA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_H36B}	vKVVTpKVET	GASPEHVsAP	AVPVTtTStA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_090}	vKVVTpKVET	GASPEHVsAP	AVPVTtTStA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_CJB110}	vKVVTpKVET	GASPEHVsAP	AVPVTtTStA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_18RS21}	vKVVTpKVET	GASPEHVsAP	AVPVTtTSpA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_2603}	vKVVTpKVET	GASPEHVsAP	AVPVTtTSpA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_JM9130013}	vKVVTpKVET	GASPEHVsAP	AVPVTtTSpA	TDsKLQATEV	KSVpVAQKAP
msa237049.2{322_1169NT}	aKVVTpKVET	GASPEHVpAP	AVPVTtTStA	TDnKLQATEV	KSVpVAQKAP
Consensus	*****	*****	*****	*****	*****
301					350
msa237049.2{322_COH1}	TAtPVAQPAS	TTNAVAAHPE	NAgLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M781}	TAtPVAQPAS	TTNAVAAHPE	NAgLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M732}	TAsPVAQPAS	TTNAVAAHPE	NAgLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_A909}	TAtPVAQPAS	TTNAVAAHPE	NArLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_H36B}	TAtPVAQPAS	TTNAVAAHPE	NArLQPHVAA	YKEKVASTYG	VNEFSTYRAG

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_090}	TAtPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_CJB110}	TAtPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_18RS21}	TAtPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_2603}	TAtPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_JM9130013}	TAtPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_1169NT}	TAtPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
Consensus	***-*****	*****	***-*****	*****	*****
351					
msa237049.2{322_COH1}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_M781}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_M732}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_A909}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_H36B}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_090}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_CJB110}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_18RS21}	DPGDHGKGLA	VDFIVGtNQA	LGnkVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_2603}	DPGDHGKGLA	VDFIVGtNQA	LGnkVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_JM9130013}	DPGDHGKGLA	VDFIVGtNQA	LGnkVAQYST	QNMAANNISY	VIWQKfYSN
msa237049.2{322_1169NT}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQKfYSN
Consensus	*****	*****-***	***-*****	*****	*****
401					
msa237049.2{322_COH1}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_M781}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_M732}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_A909}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALh
msa237049.2{322_H36B}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALh
msa237049.2{322_090}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_CJB110}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_18RS21}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_2603}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_JM9130013}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_1169NT}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
Consensus	*****	*****	*****	*****	*****-
451 460					
msa237049.2{322_COH1}	RLSRFLYNFY				
msa237049.2{322_M781}	RLSRFLYNFY				
msa237049.2{322_M732}	RLSRFLYNFY				
msa237049.2{322_A909}	RLSRFLYNFY				
msa237049.2{322_H36B}	RLSRFLYNFY				
msa237049.2{322_090}	RLSRFLYNFY				
msa237049.2{322_CJB110}	RLSRFLYNFY				
msa237049.2{322_18RS21}	RLSRFLYNFY				
msa237049.2{322_2603}	RLSRFLYNFY				
msa237049.2{322_JM9130013}	RLSRFLYNFY				
msa237049.2{322_1169NT}	RLSRFLYNFY				
Consensus	*****				

Table 70: Comparative Sequences relating to SAG 1280

SEQ ID. NO. 7001

STRAIN 2603

ATGGGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGAGCCACTATTCTC
 GTGATAGAGCCTTGCTTGAGGCATTTTATATTACCAAGCAGAGCATTTTGATGAGGAGT
 GGGATAGTCTTATTCATCAGTTTATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAG
 TACTTCACTTTGAGACAGATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTC
 ATGATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTAGATAAAC
 TATCGCCGTCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCATCTGGCCACTCGTT
 TTCAATTATTGGATTCCAATGGACACTACCAAACCATATCGCCGGATTCACTCTTACAAA
 AGAGTAGGGGAGCTAATTTGGTCAATGTGTATCGTGTGGCTAATAATTTAGCGGATCGTA
 TTAGTCGAGATATTGAACAGTTTCTCTTAACCTACGAGCCTGAGCTTGAAACTAGAGCTG
 ATGAAACTGTTCTAGAAAATGAAGAACTGTTGATGAGCACAAAACAAGTGTTCATCAAG
 CAATATCTTTTTCGAGAAGAGGCTCTCTGGTTATTGCTAGTTTGGATGTAGATTTGTCTC
 AACTAGATGTTCAAATAGGAAAAACAGTCATCTGCCAGCTTATGAAGAGTTATCCTTAC
 GACGTAAATTTGAGATTCTAACATATTTTGACCAAATTCGAAATGAACGTTCCAAAGTCC
 CAAGTTTGTAGACGAGGTGATTTTGACACAGAGATGGAAATGACACCAGTCTTTGATGGCG
 AGGAATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGCTGA
 CTACAGTCGAAGAAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGGATAGAAAAATCAAG
 AAAAATTGACTCAGCTAGGGATTGATTTATCTCAGTTTGACCCAGACCGAGTCGGTATTT
 TATTGGATGCAGCAGGTGTTTTCTGTTTAAAAAATGCAGACCTTGTCTTACTAGGTGGTT
 ATCCCAAAGCCTCGGTAACCTCACTAGCCCTTGGCAGACAACTACTCCAAATGGGACTAA
 GTCATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTGCGACAAG
 TTGCCTACGCCTTTTATACCAAGAACTCAGCAGAGAAGATGCGGAGCAATTTGAAAAAG
 ATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTGGAAGCAAGCTAGAGAAAGCTG
 AGGGAAGAAGTAGTTGATGAAGAATTCGCGGAAAATCCACTGGTTTCAGAGAGTATTGG
 ACCTTATCCTCTGGGGTCATTGGTTTTCTATAAGGGACAGGACTTTGAGGTGATGTCGG
 TCAGCGATGCTCGATTGAACGGTTTGATTGCGATTGAGTTAGTCAATGACTTTTTCGGATA
 TCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGAGTCAAGTCAGGCACCTC
 ATCAGCCAAAGGCAGAACCAACAGAGTTAGAAGAAGCGGACCAAGAAATTAACCTAT
 TCTCATTCTGGAAGAGGAGCCAGTTGAGATTTGGACTATTGGAACCAGATGATTGAG
 AAAATGGTCATAACGATACTGATCTTGAAGAAAACAGATAATCAAAATTCCTGAAGAGGAAG
 TCGTCGAAACAATTCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGACGG
 ACTTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTGGCCATTCTGTTGG
 TAAAAAATCTAGAAGTAGAGCACCGCAATGCTTCACCAAGTGAACAAGAACTCCTTGCCA
 AGTATGTAGGCTGGGGTGGACTAGCCAATGAATTTTGTGATGACTATAATCCAAATTTT
 CTAAGGAACGAGAAGAACTGAAGAGCCTATCACAGATAAAGAGTATTCGGATATGAAAC
 AGTCCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTCAGATGTGGGATAAGT
 TGGAAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATGGGAACAGGGAATT
 TCTTTGCGGCTATGCCAAAACACTTAAGAGAAAAGAGTGAGTTGTATGGCGTAGAGTTAG
 ATACTATTACAGGAGCTATTGCCAAAACACCTTCATCCCAATAGTCAATTTGAAATTAAGG
 GATTTGAGACGGTGGCTTTTAACGACAATAGTTTTGATTTGGTGATTTCAAATGTGCCCT
 TTGCCAATATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTGATGACTACT
 TTGTCAAAAAGTCACTTGATTGCTTTCATGATGGTGGACAAAGTAGCGATTATCTCTTCCA
 CAGGAACATATGGATAAGCGAACAGAAAACATCTTACAAGATATTCTGTGAGACAACTGAAT
 TTCTTGGTGGGGTTGACTGCTGACTCTGCCCTTAAGGCCATTGACGGAACGAGTGTCA
 CAACGGATATGTTATTCTTCCAGAAAACACTTAGACAAGGGATATGTGGCAGACGATTTAG
 CCTTTTCAGGTTCCATTGCTATGACAAGGATAGTTCGCTTTGGCTCAATCCTTATTTTG
 ATGGAGAATACAAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAATTTTAACGGAGGAA
 CACTTTCTGTGTTAAGGGGACTAGTGATGACTTGATTGCAAGTGTGAAAACAGCTCTAAATC
 ACGTTAAGGCCCCAAGAGAGATTGATAGAAATGAGGTGATCATTAAACCCAGATGTGTTGA
 CCAAACAAGTCAATGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACA
 GTTTTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCAGTCCGGA
 CCAAGACGGAAGAAATCAGTTACTATGTGATGAAGAGGGCAACTTCAAAGCATGGGACA
 CCAACATTCTCAAAAGCAGATTGATCGCTTAAATGCTTGAAGTGAAGTGAATAACACTG
 CTCTGGATGTCTATGTGACCGATGATGCAGCCAAACGTGGTCAAGTTTAAAGGGTATTATA
 AAAAGACAGTTTTCTATGAAGCTCCATTGTCTTATAAAGAAGTGGCACGTATCAAAGGAA
 TGGTCGATATTTCGCAATGCTTACCAAGAAGTTATTGCCATTCAACGCTATTATGACTATG
 ATAAGGAGACCTTTAACCCTTGTAGGCAAACTCAATCGTACCTATGATAGCTTTGTCA
 AACACTATGGGTATTGTAATAGTGTGTGAACCGCAATCTTTTGTAGTGTATGATAAGT
 ATTCTGCTTTCTGTGATTTGGAAGATGAAAGTCTGGATCCAAAGTGGAAAGTCTGTTATCT
 ATACTAAATCCCTTGCCCTTTGAGAAGGCTCTAGTGGCTCCTGAAAAAGAGGTAAAAAGG
 TGCATACTGCCCTTGATGCCCTTAAATTCGAGCTTGGCTGACGGACGAGGTGTTGATTTCCG
 CTTATATGATGTCTATCTATCAGGTGAATCGCAGATGACCTTGATTGAGGAGTTAGGCG
 ACCTCATTATGCTGATCCTGAGAAATTTGAATGGAGAATTGACCTATGTTTCTCGCC
 AAGACTTTCTTTGAGGGGATGTCGTCATAAGTTAGAAGTGGTAGATCTATTCGTCAAAC
 AAGACAATCAGGACTTTAACTGGTCACATTATGCGGGACTTCTAGAAGCTATCAAACCAG
 CCCGTATTACTTTGGCAGACATTGATTATCGAATCGGTTTACGCTGGATTCTCTGGCTG
 TTTATGAAAAATTTGCCCAAGAAACCTTTATGGGGAAAGCCTATGAACTGTCAGACCAAG
 AAGTAGCGACAGTCTTAGAAGTCAATCCATTGACGGGGTTATCACTTACCAATCTAAGT
 TTGCCTACACCTATTCCAACGCAACGGATAGGAGTTTAGGTGTCCTGCTTACGCTATG
 ATAGTGGTCGAAAAATCTTTGAAAAATCTCTGAATTTCCAATCAACCAACCATCACAAAAC
 AAGTTGTGCAAGGGGATAAGAAAAAGAATGTGACGGATGTAGAGAAAACAACGGTCTGTC
 GTGCCAAGGAAACACACCTACAAGAACTCTTTCAAGGTTTGTAGCAAAGTATCCAGAAG
 TCCAACAAATGATTGAAGACACCTATAATAGGCTCTACAATCGTACGGTATCAAAGTCCT
 ATGATGGTAGTCATTAAACCATGATGGACTTGTCTCAGAATATCTCCTTACGTCCTCACC
 AAAAGAATGCCATTCAACGAATTGTGCGAGGAAAAACGTGCTCTACTAGCTCATGAAGTTG
 GTTCAGGTAAAAACACTTACCATGCTTGGGGCAGGATTCAAACGAAAGAACTCGGAATGG
 TACATAAACCACCTTTATGTGGTGCCGTCTAGTCTGACTGCTCAGTTTGGTCAAGAAATCA
 TGAAATTTTCCCTACCAAGAAAGTCTATGTGACTACTAAGAAAGACTTTGCCAAAGCCA
 AACGCAAGCAGTTTGTGTCCCGTATTATTACAGGGGACTATGATGCCATTGTCTATTGGGG
 ATTACAAATTTGAGAAGATACCGATGAGTCTGAAAAACAGGTACCTATATCAATGACA
 AACTTGAGCAACTCCGAGAAATCAAGCTAGGAAGTGACAGTGATTACACGGTGAAAGAAG
 CGGAACGTTGATTAAGGGATTAGAACACCAGTTGGAAGAACTCCAAAACTAGAGCGAG